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Copyright (c) 1993 - 2002 Compugen Ltd
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Q9nrr4 homo sapien
Q9nrr4 homo sapien
Q01326 caenorhabdi
P51833 bacillus su
Q9kpb2 vibrio chol
P57805 pasteurella
Q9ka05 bacillus ha
P13983 nicotiana t
P57346 buchnera ap
Q9chd0 lactococcus
P05797 escherichia
P49750 homo sapien
Q9fpq6 chlamydomon
Q9fpq6 chlamydomon
Q9fpq7 streptomyce
Q51648 borrelia buv
P55439 drosophila
Q50656 salmonella
P74368 synechocyst
Q9zbq7 streptomyce
Q51648 borrelia buv
Q53627 rattus norv
P56118 helicobacte
Q95104 homo sapien
Q53844 spiroplasma
P44441 haemophilus
Q9zbq7 shlamydia m
P54258 rattus norv
Q9xcxy pseudomonas
Q9xh27 homo sapien
P34259 rchlamydia m
P51532 homo sapien
Q3x9787 treponema p
Q15427 homo sapien
P12978 epstein bar
Q9zcc7 chlamydia p
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218	218	218	220.5	221	222	222.5	223	223.5	223.5	225	225.5
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Q14687 homo sapien										084299 chlamydia t	-

## ALIGNMENTS

SEQUENCE OF 706-1374 FROM N.A.  TISSUE-AOTTA; Wei Y.J., Ding J.F., Xiong H., Zhou Y., Liew C.C. Submitted (DEC-1998) to the EMBL/GenBank/DDBJ dat -!- FUNCTION: Involved in pre-rRNA processing. Cl RNA and does not cleave single-strand RNA!- CATALYTIC ACTIVITY: Endonucleolytic cleavage phosphomonoester!- SUBUNIT: Interacts with Spl!- SUBCELLULAR LOCATION: Nuclear. A fraction is nucleolus during the S phase of the cell cycl -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown he produced by alternative splicing!- TISSUE SPECLFICITY: Ubiquitous!- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED	SEQUENCE OF 603-1374 FROM N.A.  TISSUE-Embryo; Isogai T., Ota T., Hayashi K., Sugiyama T., O' Isogai T., Ota T., Hayashi K., Sugiyama T., O' Nishikawa T., Nagai K., Sugano S., Shiratori i Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H. Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H. Takahashi M., Chiba Y., Ishida S., Murakawa K Takahashi M., Chiba Y., Ishida S., Murakawa K Watanabe S., Kimura K., Murakami K., Ishii S., Yamamoto J., Wakamatsu A., Nakamura Y., Nagah Ninomiya K., Iwayanagi T.; "NEDO human cDNA sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ	SEQUENCE FROM N.A. (ISOFORM 1).  SEQUENCE FROM N.A. (ISOFORM 1).  MEDLINE=20538440; PubMed=10948199;  Wu H., Xu H., Miraglia L.J., Crooke S.T.;  "Human RNase III is a 160-kDa protein involved in processing.";  J. Biol. Chem. 275:36957-36965(2000).  [2]  SEQUENCE OF 166-613 FROM N.A. (ISOFORM 2).  TISSUE-Colon;  MEDLINE=20431278; PubMed=10976766;  Gunther M., Laithier M., Brison O.;  "A set of proteins interacting with transcription identified in a two-hybrid screening.";  Mol. Cell. Biochem. 210:131-142(2000).	RNC_HUMAN  ID RNC_HUMAN  ID RNC_HUMAN  ID RNC_HUMAN  ID RNC_HUMAN  ID RNC_HUMAN  AC O9NRR4; Q9NW73; Q9Y2V9; Q9Y4Y0;  DT 01-MAR-2002 (Rel. 41, Created)  DT 01-MAR-2002 (Rel. 41, Last sequence update)  DT 01-MAR-2002 (Rel. 41, Last annotation update)  DE Ribonuclease III (EC 3.1.26.3) (RNase III) (p241).  GN RNASE3L OR RN3.  OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;  CC Mammalla; Eutherla; Primates; Catarrhini; Hominidae;  NC NCBL_TaxID-9606;
C.C.; J databases. g. Cleaves double-strand A. vage to 5'- vage to 5'- vage to 5'- vage to 5'- n is translocated to the cycle. wn here) and 2; may be NDED RNA-BINDING) DOMAIN.	Otsuki T., Suzuki Y., A., Sudo H., ., Kondo H., Sugawara M., K., Ono Y., Takiguchi S., ., Kawai Y., Salto K., hari K., Masuho Y.,	<b>⊢•</b>	p241). p241). ebrata; Euteleostomi; minidae; Homo.

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EMBL; AJ242976; CAB45133.1; -.

EMBL; AJ242976; CAB45133.1; ALT_INIT.

EMBL; AF001121; BAA91511.1; ALT_INIT.

EMBL; AF116510; AAD29637.1; ALT_FRAME.

InterPro; IPR000159; DS_RBD.

InterPro; IPR000359; RISSER

Pfam; PF00035; GSRM; 1.

Pfam; PF000536; RIBONICLEASE_3; 2.

SMART; SM00535; RIBOC; 2.

PROSITE; PS50137; DS_RBD; 1.

PROSITE; PS50137; RNASE_3_1; 2.

PROSITE; PS50142; RNASE_3_2; 2.

PROSITE; PS50142; RNASE_3_3; RNASE_III 2.

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                       KRARWEEEKDRWSDNQSSGKDKNYTSIKEKEPEETMPDKNEEEEEELLKPVWIRCTHSEN
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RNASE III 1.

RNASE III 1.

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ISOFORM 2).

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YQYPPGYSH -> RERERTSLE (IN REF. 2).

L -> P (IN REF. 2).

L -> P (IN REF. 1).

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                                                     KARRIGIRHSIYPGEEAIKPCRPMTNNAGRLFHYRITVSPPTNFLTDRPTVIEYDDHEYI
                                                                                                                                                                                                                                                          YYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKAKAARPPWEPPKTKLDEDLESS
    EMGAAMDALEKYNFPQMAHQKRFIGRKYRQELKEMRWEREHQEREPDETEDIKK
                                   RINHNERLEFLGDAVVEFLTSVHLYYLFDSLEEGGLATYRTAIVQNQHLAMLAKKLELDP
                                                                                                                                                                                  KARRTGIRHSIYPGEEAIKPCRPMTNNAGRLFHYRITVSPPTNFLTDRPTVIEYDDHEYI
                 RINHNERLEFLGDAVVEFLTSVHLYYLFPSLEEGGLATYRTAIVQNQHLAMLAKKLELDR
EMGAAMDALEKYNFPQMAHQKRFIERKYRQELKEMRWEREHQEREPDETEDIKK
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RESULT 2

RNC\_CAEEL STANDARD; PRT; 10

ID RNC\_CAEEL STANDARD; PRT; 10

AC 001326; 001327; Q9U9Q8;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence up
DT 01-MAR-2002 (Rel. 41, Last annotation
DE Ribonuclease III (EC 3.1.26.3) (RNase

1086 AA

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Matches 364
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SMART; SM00535; RIBOC; 2.
PROSITE; PS0137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1; 2.
PROSITE; PS0142; RNASE_3_2; 2.
Ribosome biogenesis; Hydrolase; Nuclease; RNA-binding; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 227-1086 FROM N.A.
MEDLINE-20179701; PubMed-10713462;
Filippov V., Solovyev V., Filippova M., Gil
"A novel type of RWase III family proteins
Gene 245:213-221(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: Involved in pre-rRNA processing. Cleaves double RNA and does not cleave single-strand RNA (By similarity)
-i- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lightning
Submitted
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Submitted
                                                                                                                                                                                                                                                                                     RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F26E4.10 OR F26E4.13.
Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF160248; AAD45518.1; WormPep; F26E4.10; CE09694.
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STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001159; DS_RBD.
InterPro; IPR000999; RNase_3
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364;
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SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING)
SIMILARITY: CONTAINS 2 RNASE III DOMAINS.
                                                                                                                                        KHKRARRKKYQKEYQERHKEEMMQQLGRRFQNQPSTSSAPPDTVEKIPLPTESTSALPFG
                                                                                                                                                                 RHRSYERSRERERHRHRDNRRSPSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELP-G
                                    AEEAEKYMMIKAKSTTSKILQDFQTKILETVKTKRRLQADVPYIIHPCHSMKGRKTPKQK
                                                   EKEPEETMPDKNEEEEEELLK----
                                                                                       DSPRLTEKDYETNYMIDPP - - VVSTHSAELIK - - -
                                                                                                               EIIKNTDS-----WAPPLEIVNHRSPSREKKRARWEEEKDRWSDNQSSGKDKNYTSIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z81070; CAB03006.3;
                                                                                                                                                                                           Similarity 31.2
64; Conservative
ENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKAKAARPP--WEPPKTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.;
(OCT-2001)
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(OCT-1996)
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AAD45518.1; -.
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                                                                                                                                                                                           Score 1448; DB 1;
Pred. No. 5.7e-65;
)6; Mismatches 431;
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RNC\_BACSU
ID RNC\_B
AC P5183
DT 01-OC
DT 30-MA

RNC\_BACSU STANDAR P51833; O31734; O1-OCT-1996 (Rel. 34, 30-MAY-2000 (Rel. 39,

Last Created)

sequence update)

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                                                                                                                                                       AALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLR-TEGKEPDIPLY 1284
                                                                                                                                                                                                                                                                                         EFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQLVATEYLFIHFPD 1168
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                              GRKYROELKEMRWEREHOEREPDETED
                                                                 RVLGIEGPTNNRIFKIAVYYKGKRLASAAESNVHKAELRVAELALA-
                                                                                                                                   GALYVDRGIEHCRAFIRIVFCPRLKHFIESEKWNDAKSHLOOWCLAMRDPSSSEPDMPEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVQLWSSKTVLAYFTSKGSSEIMSPEDVNRLCDAQIDQFTRNTSKHKQSIVLNTKFKPSA 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EFMPDECFDPEDCDMLFEYIFHEIFEMLDFELRPKHIPSDVESCPMIHIMPRFVQ-TKDD 430
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-MKAKNNSWFQNMRRRLEQDTSD
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Matches 85
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InterPro; IPR000999; RNase_3.
Pfam; PP000035; dsrm; 1.
Pfam; PP00035; Ribonuclease_3; 1
SMART; SM00358; DSRM; 1.
SMART; SM00535; RIBOC; 1.
                                                                                                                                                                                                                                   1104
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Submitted (NOV-1997) to the EMBL/GenBank/DBB databases.
-!- FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED IN THE PROCESSING
OF RIBOSOMAL RNA PRECURSORS AND OF SOME MENAS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
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[2]
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"The effect of Srb, a homologue of
subunit, on Bacillus subtilis grow
Gene 172:17-24(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus/Staphylococcus
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
Bacteria; Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CTUTTARTTY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING)
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                                                                                                                                                                                                                                LQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGH--NQRMEFLGDSIMQLVATEY 1161
                                                                                                                                                                                    VEQFKEFQERISVHFQNEKLLYQAFTHSSYVNEHRKKPYEDNERLEFLGDAVLELTISRF
FEAFIGALYLDQGLEPVESFLKVYVFPKINDGAFSHVM-DFKSQLQE----YVQRDGKGSL
                                         LESFIAALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLRTEGK---
                                                                                          LFAKYPAMSEGDLTKLRAAIVCEPSLVSLAHELSFGDLVLLGKGEEMTGGRKRPALLADV 136
                                                                                                                                                                                                                                                                                                                                                                                 JSRM; 1.

JSS, RIBO; 1.

PS50137; DS_RBD; 1.

PS50142; RNASE_3_1; 1.

PS50142; RNASE_3_2; 1.

PS00517; NASE_3_2; 1.

PS00517; NASE_111

PS005142; PRASE_111

PS005142; PRASE_111

PS005142; PRASE_111

PS005142; PRASE_111

PS005144; PRASE_111

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                                                                                                                                                                                                                                                                                 46;
                                                                                                                                                                                                                                                                                                       Score 315; DB 1;
Pred. No. 2.3e-09;
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-> P (IN REF. 1).
-> E (IN REF. 1).
-> QLNPPYDSGGFQYVCRLI (IN REF.
304F3BOBF5B7CCDC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 406:477-483(2000).
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STRAIN=EL TOR N16961 / SEROTYPE O1
MEDLINE-20406833; PubMed-10952301;
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16-OCT-2001
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                                                                                                                  PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1; 1.
PROSITE; PS50142; RNASE_3_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               phosphomonoester.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
-i- SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
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16-OCT-2001
                                                                                                     Hydrolase;
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InterPro; IPR000999;
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                                                                                                                                                                                            PF00035; dsrm; 1.
PF00636; Ribonuclease_3;
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 Similarity 32.75; Conservative
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                                                          Nuclease; Endonuclease;
5 127 RNASE
154 224 DRBM.
225 AA; 25010 MW; 6921
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E III (EC 3.1.26.3) (RNase III).
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   42;
Score 285.5; DB
Pred. No. 6e-08;
42; Mismatches 1
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                                                           692FEE74C580990C CRC64;
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                                                                                        III.
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May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., K.
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
1- FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED IN THE
OF RIBOSOMAL RNA PRECURSORS AND OF SOME MENAS (BY SIMIL-
1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
              1105 QKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQLVATEYLFI 1164
                                                                                                                                                                                SMART; SM00358; DSRM; 1.
SMART; SM0535; RIBOC; 1.
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1; 1.
PROSITE; PS50142; RNASE_3_2; 1.
                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
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16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat Ribonuclease III (EC 3.1.26.3) (RNase III).
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                                                                                                                         SEQUENCE
                                                                                                                                                        Hydrolase; Nuclease; Endonuclease; RNA-binding; Complete proteome DOMAIN 5 127 RNASE III.
                                                                                                                                                                                                                                                           Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3;
                                                                                                                                                                                                                                                                                           InterPro; IPR001159; InterPro; IPR000999;
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Pasteurella.
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SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
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 QNLERLQRQIGYQFNQPALLKQALTHRSA----
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                                                                           Similarity
                                                                                                                        225 AA;
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                        25461 MW;
                                                                         3.8%;
                                                                                                                                                                                                                                                                                                               DS_RBD
                                                                                                                                                                                                                                                                                             RNase_3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma subdivision; Pasteurellaceae;
                                                            44;
                                                                        Score
Pred.
                                                                                                                                     DRBM
                                                                                                                                                   RNASE III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                1
                                                                                                                      202B6ACCA562B31C CRC64;
                                                           Mismatches
                                                                         282;
No. 8.
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-AVKHNERLEFLGDAILNFIIAEALYH
                                                                         DB 1;
.9e-08;
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                                                           101;
                                                                                      Length 225;
                                                           Indels
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                                                           12;
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                                                         Gaps
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RESULT 6
RNC_BACHD
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Query Match
Best Local S
Matches 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                              SMART; SM00358; DSRM; 1.
SMART; SM00355; RIBOC; 1.
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1;
PROSITE; PS50142; RNASE_3_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the alkaliphilic bacterium Bac halodurans and genomic sequence comparison with Bacillus su Nucleic Acids Res. 28:4317-4331(2000).

-I- FUNCTION: Digests double-stranded RNA. Involved in the of ribosomal RNA precursors and of some mRNAS (By simil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Ribonuclease III (EC 3.1.26.3) (RNase III).
                                                                                                                                                                                                                                    EMBL; AP001515; BAB06208.1; -.
InterPro; IPR001159; DS_RBD.
                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9KA05;
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                                                           SEQUENCE
                                                                        DOMAIN
                                                                                       DOMAIN
                                                                                                                                                                                       Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3;
                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRA-!- SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN

    -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takami H., Nakasone K., Takaki Y., Maeno G.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNC OR RNCS OR BH2489.
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                                                                                                    Hydrolase;
                                                                                                                                                                                                                    InterPro; IPR000999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphomonoester.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKTLQTVGPSHARTYTVAVYFKG-ERIGCGKGPSIQQAEMGAAMDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IIGAISLDSDLATTKIVQHWYQAQLKQIQPGDNQKDPKTRLQE-----YLQGKRLPLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIAALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLRTEGKEPDIPL 1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OFPKCNEGELSRMRATLVREPTLASLARQFELGDYLSLGPGELKSGGFRRESILADCVEA 117
Similarity
77; Conserv
                                                                                                    Nuclease; Endonuclease;
                                                           263
 Conservative
                                                                        190
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                                                           AA;
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                                                         164 R
259 E
30224 MW;
             3.8%;
                                                                                                                                                                                                                     RNase_3.
 50;
Score 282; DB
Pred. No. 1.1e
50; Mismatches
                                                                       DRBM.
                                                                                      RNASE III.
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                                                           61B8E1C557CC5485
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                              DB
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                1e-07;
   110;
                                                                                                                                                                                                                                                                                                         Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sasaki R.,
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                                                           CRC64;
                                                                                                    Complete proteome.
                            Length
 Indels
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                              263;
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                                                                                                                                                                                                                                                                                                                                                      EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                      a collaboration
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1084 HPLQLQEPNTDRQLIETSPVLQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNH--LTLG 1141

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                           REPEAT
DOMAIN
REPEAT
REPEAT
DOMAIN
                                                                                                                                                                                                                                                                           This SWI
                                                                                                                                                                                                                                                                                                                                                                                   Keller B., Lamb C.J.;

"Specific expression of a novel cell wall hydroxyproline-rich glycoprotein gene in lateral root initiation.";

Genes Dev. 3:1639-1646(1999).

"I- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicotiana tabacum (Common tobacco).

Ricotiana tabacum (Common tobacco).

Ricotiana; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last anotation update)
Extensin precursor (Cell wall hydroxyproline-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _TOBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1142
                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=CV. XANTHI; TISSUE=Leaf;
MEDLINE=90128263; PubMed=2612909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1261
                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1202
                                                                                                                                                                    PIR;
                                                                                                                                                                              EMBL; X13885; CAA32090.1;
                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HRGPNT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P13983;
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 SEQUENCE
                 DOMAIN
                                                                                                 REPEAT
                                                                                                                           SIGNAL
                                                                                                                                       Hydroxylation.
                                                                                                                                                   Repeat;
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                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Extracellular matrix. PTM: EXTENSINS CONTAIN A CHARACTERISTIC REF
                                                                                                                                                    S06733; S06733
at; Cell wall; (
                                                                                                                                                                                                                                                                                                                    GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                 SER-PRO(4). THE
                                                                                                                                                                                                                                                                                                                                                                         MAIN ROOT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGKGEEMTGGRKRPALLADVFESFVGALYLDQGMDAVYLFLERTIYPKISEGAFSH-MMD
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21
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148
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                            20
620
73
151
242
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                                                                                                                                                   Glycoprotein; Signal;
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  65406
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                                                                   POTENTIAL.
EXTENSIN.
H-A-P-P.
H-A-P-P.
2 x 7 AA T
 CONTAINS THE SER-PRO(4) REPEATS 3 X APPROXIMATE TANDEM REPEATS.; 641DD2278AB28524 CRC64;
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is
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RESULT 8
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Best Local
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16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-20445173, PubMed-1093077; Shigenobu S., Watanabe H., Hattori M., Sakaki Y "Genome sequence of the endocellular bacterial Buchnera sp. APS."; Nature 407,81-86(2000).
SMAKI; SMAKI; SMAKI; DS_RBD; 1.
PROSITE; PS00137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1; 1.
PROSITE; PS50142; RNASE_3_2; 1.
undrolase; Nuclease; Endonuclease;
                                                            Pfam; PF00035; dsrm; 1.
pfam; PF00636; Ribonuclease_3;
SMART; SM00358; DSRM; 1.
SMART; SM00535; RIBOC; 1.
                                                                                                                                                                                                    the European Bioinformatics Institute. There are no resuse by non-profit institutions as long as its content modified and this statement is not removed. Usage by a
                                                                                                                                                                         or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
NCBI_TaxID=118099;
                                                                                                                    InterPro; IPR001159;
InterPro; IPR000999;
                                                                                                                                   EMBL; AP001118; BAB12968.1; InterPro; IPR001159; DS_RBD
                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                     phosphomonoester.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
-i- SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-TOKYO 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   symbiotic bacterium).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNC OR BU258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribonuclease
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                                                                                                                                                                                                                                                                                                                                             FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED IN THE PROCESS OF RIBOSOMAL RNA PRECURSORS AND OF SOME MRNAS (BY SIMILARITY). CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
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                                                                                                                                                                                                                                             the Swiss Institute of Bioinformatics
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
e III (EC 3.1.26.3) (RNase III).
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Best Local
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Q9CHDO;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 40, Created)
01-MAR-2001 (Rel. 40, Created)
01-MAR-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial contents are not as a statement of the commercial contents and the statement is not removed.
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SMART; SM00358; DSRM; 1.
SMART; SM00535; RIBOC; 1.
PROSITE; PSS0137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1;
PROSITE; PS50142; RNASE_3_2;
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DOMAIN
                                                                                   InterPro; IPR000999; RNase_3. Pfam; PF00035; dsrm; 1. Pf00636; Ribonuclease_3;
                                                                                                                                          EMBL; AE006313; AAK04900.1; -.
InterPro; IPR001159; DS_RBD.
                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Cytoplasmic (By si-
-i- SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRA
-i- SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of the lactic lactis ssp. lactis IL1403."; Genome Res. 11:731-753(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21235186; PubMed=11337471;
Bolotin A., Wincker P., Mauger S.,
Weissenbach J., Ehrlich S.D., Soro
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                                                                                                                                                                                                               entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: Endonucleolytic
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Racteria: Firmicutes; Bacillus/Clostridium
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                                                                                                                                                                                             send an email to license@isb-sib.ch).
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  SEQUENCE FROM N...
SEQUENCE FROM N...
STRAIN=K12 / MG1655;

MEDLINE-9746617; PubMed-9278503;

MEDLINE-9746617; PubMed-9278503;

MEDLINE-9746617; PubMed-9278503;

Blattner F.R., Plunkett G. III, Bloch C.A., Poiley M., Collado-Vides J., Glasner J.D., Ro
Piley M., Collado-Vides J., Glasner J.D., Ro
                                                                                                       Nashimoto
Submitted
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P05797; PO
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SEQUENCE
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01-JAN-1988 (Rel. 06, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Ribonuclease III (EC 3.1.26.3) (RNase
RNC OR B2567 OR Z3848 OR ECS3433.
Escherichia coli, and
                                                                                                                              STRAIN-K12;
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                                                                                                                                                                                                         STRAIN=K12 / SB221;
MEDLINE=85269601; P
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                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                            Escherichia coli.";
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-86039802;
                                                                                                                                                                                                                                                                                                                                                           Escherichia
                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli 0157:H7.
                                                                                                                                                                 Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                 Nashimoto H., Uchida
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562,
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76; Conserv
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                                                                                                       H., Saito I
(SEP-1995)
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231 AA;
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26137 MW;
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31.3%;
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                                                                                                                                                                                                                                                                                     Escherichia
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                                                                                                                                                                                      gene (rnc) encoding ribonuclease
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Escherichia coli
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                     Perna N.T., Burlode C.K., Mayhew eden M.A., Rose I
                                                                                                                                                                                                                                                                                                                                                                      Enterobacteriaceae;
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Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-0157:H7 / RIMD 0509952;

MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science [5]
                                                                                                                                              EMBL;
                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 211-226 FROM N.A.
SEQUENCE OF 211-226 FROM PROPERTY OF SECUENCE AND J., March P.E., Takiff H.E., Inou
"A GTP-binding protein of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-45 EMEDLINE=89213943; Takiff H.E., Chen
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[6]
                            PIR; A24022; NREC3.
ECGGENE; EGG10857; rnc.
InterPro; IPR0011159; DS_RBD.
InterPro; IPR000999; RNase_3.
Pfam; PF00035; dsrm; 1.
Pfam; PF00636; Ribonuclease_3; 1.
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[7]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriol.
                                                                                                                          BL; AE000343; AAC75620.1; -.
BL; AE005487; AAG57682.1; -.
BL; AF002562; BAB36856.1; -.
BL; MA6415; AAA21843.1; -.
BL; M14658; AAA03241.1; -.
BL; AAA023; NREC3V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C. Natl. Acad. Sci. U.S.A. 83:8849-8853(1986).
FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED IN
OF RIBOSOMAL RNA PRECURSORS AND OF SOME MRNAS.
CATALITIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF RNA-PROCESSING ENZYMES.
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: CONTAINS 1 DREM (DOUBLE-STRANDED RNA-BINDING) DOMAIN
SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphomonoester
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                                                                                                                                                                                                                            X02946; CAA26692.1; -. X02673; CAA26504.1; -. D64044; BAA10914.1; -. U36841; AAA79829.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .E., Chen S.M., Court D.L.;
analysis of the rnc operon of Escherichia
riol. 171:2581-2590(1989).
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8:11-22(2001).
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RIBOC; 1.
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chia coli has homology
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Best Local S
Matches 70
                                                                                                                     A Sherrington R., Rogaev E.I., Liang Y., Rogaeva E.A., Leves I Reda M., Chi H., Lin C., Li G., Holman K., Tsuda T., Mar Foncin J.-F., Bruni A.C., Montesi M.P., Sorbi S., Rainero A Pinessi L., Nee L., Chumakov I., Pollen D., Brookes A., Sanseau P., Pollinky R.J., Wasco W., da Silva H.A.R., Hain Pericak-Vance M.A., Tanzi R.E., Roses A.D., Fraser P.E., Rommens J.M., St George-Hyslop P.H.;

"Cloning of a gene bearing missense mutations in early-ons Alzheimer's disease.";

Latheimer's disease.";

Latheimer's disease.";

Latheimer's disease.";

Latheimer's disease.";

Latheimer's disease.";

Latheimer's disease.";
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DOMAIN
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Eukaryota; Metazoa; G
Mammalia; Eutheria; P
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                                                                                               frameshift in position 1661.
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PS00517;
PS50142;
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44
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); RNASE_3_1; 1.
); RNASE_3_2; 1.
); RNASE_12; RNASE I 128
RNASE I 128
DRBM.
44
G->D: L
HLPLPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Primates;
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Pred. No. 8
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HLPLPTKILVYOVRGEAHDQEFTIHCQVS -> PSAAADI
SPGTWSKTIRNLLSTRAFY (IN REF. 2).
D9E2858F2E0AA3A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         asi N., Baradarani L., Birditt
Fleetwood P., Harrison G., Jan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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III.
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n K., Tsuda T., Mar L.,
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A., Shaffer T.,
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DOMAIN 1488
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CONFLICT 1821
SEQUENCE 1822 A
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                                                                                                                                                        HSIYP-----GEEAIKPCRPMT------NNAGRLFHYRITVSPPTNFLTDRPTVIEYDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGRGCPRGRGGHG----ARPSAP-----SFRPQNL----RLLHPQQPPVQYQYEPPSAP
                                                                                                 HEYIFEGFSMFAHAPLTNIPLCKVIRFNIDYTIHFIEEMMPENFCVKGLELFSLFLFRDI
                                                                                                                                YSSFSSDQGLGESSAAPSQPITAVKDMPVRSGGLL-----PDPPRSSYLESPRGPRFDG
                                                                                                                                                                                                      QSSQVPEKPRPALLPTPVSFGSAPPTTYH-----
                                                                                                                                                                                                                                 SDSEVFD-----VIAEIKRKKAHPDRLHDELWYNDPGQMNDGPLCKCSAKA--RRTGIR
                                                                                                                                                                                                                                                                  KHTQLQQILQQYQQIIQPPPHIQATTPPPGIPP-----PGVPQGIPPQLTAAPVPPASSS
                                                                                                                                                                                                                                                                                                   GTSRLRDLYDKFEEELGSRQEKAKAARPPWEPPKTKLDEDLESSSESECESDEDSTCSSS
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                                 LELYDWNLKGPLFEDSPPCCPRFHFMPRFVRFLPDGGKE---VLSMHQILLYLLRCSKAL
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L40400; AAC42006.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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     RPKGPRFEGNRPDGPR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARG-RICH.

P -> S (IN REF. 2).

T -> I (IN REF. 2).

K -> E (IN REF. 2).

MW; 8E6CB83FE540C7D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO-RICH.
GLN-RICH.
ARG-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long a
modified and this statement is not removed.
entitles requires a license agreement (See l
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (H
                                                                                                                                                                                                                                                                                                   InterPro; IPRO03882; Pistil_extensin.
InterPro; IPRO02965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoprotein 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. PubMed=11258910;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Associates with GP2 and GP3. PTM: N-glycosylated and O-glycosylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FKMQSAAFSIAADVKDVKAAQSNENLSDSQQEPPK
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  l Similarity
82; Conserv
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399
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                        3.5%;
                                                                                                                                                                                                                                                                                Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                       ALT_SEQ
                                                                                         VEGETATIVE CELL WALL PROTEIN GP1.

49 X 5 AA APPROXIMATE PPSSX REFEAT:
POLY-PRO.
N-LINKED (GLCNAC. . .) (POTENTIAL)
M-; 6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Waffenschmidt S.,
                        Pred. No. 3.
                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlorophyceae;
                          .5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₹
                                             DB 1;
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                                                                                                                 (POTENTIAL)
                                                                                                                                                               (POTENTIAL)
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Best Local
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misawa K., Nosaka T., Kitamura T.;
"A huge nuclear protein.";
"A huge nuclear protein.";
protein zap3 and zap11:";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear protein ZAP3. ZAP3 OR ZAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Fetal liver;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear protein.
DOMAIN 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZAP3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
  104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MGI:1926195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASR 410
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                                                    LSSATPPPGIPPPGAPQGMPPQLTAPLPPASGSQNSQIPEKPRQALLPTPVSFGSTPPSP
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925
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1012
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21.5%;
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Last annotation update)
                                                                                                                                                                                                                                                      39;
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                                                                                                                                                                                                                                                                                                                                                                                                         PRO-RICH.
GLN-RICH.
                                                                                                                                                                                                                                                                              Score 259.5;
Pred. No. 1e
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                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                            CRC64;
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                                                                                                   ----PI----RPPFP 103
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RESULT 14
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
A Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Brandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
Chen J., Botchan M.R., Downes M., Dugdan-Rocha S., Dukov B.C., Dunn P.,
A Dodson K., Doup L.E., Downes M., Dugdan-Rocha S., Dukov B.C., Dunn P.,
Davies M., Davies S., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P25439; Q9VUW5; Q9VUW6; O1-MAY-1992 (Rel. 22, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Homeotic gene regulator (Brahma protein)
BRM OR CG5942 OR CG18438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (LONG ISOFORM). MEDLINE=92154670; PubMed=1346755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Etaryota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
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                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Brahma: a regulator of Drosophila homeotic related to the yeast transcriptional activat
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Thegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Wesherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Syler E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.",
Science 287:2185-2195(2000).
CC
-i- FUNCTION: MAY ACT AS COACTIVATOR, ASSISTING ONE OR MORE DEDICATED
TRANSCRIPTIONAL ACTIVATORS OF ANT-C AND BY-C HOMEOTIC GENES. CAN
CC
-i- SUDGELULAR LOCATION: Nuclear.
CC
-i- SHORT FORM; MAY BE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC
-i- DEVELOPMENTAL STREES PRODUCED BY ALTERNATIVE SPLICING.
C- LARLY EMBRYOS.
CHARLY EMBRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001487; Bromodomain.
InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicase_C.
InterPro; IPR000330; SNF2_N.
InterPro; IPR000330; SNF2_N.
InterPro; IPR000031; Bromodomain; 1.
InterPro; IPR000271; Belicase_C; 1.
InterPro; IPR00176; SNF2_N; 1.
INTERPRO; 
                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
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EMBL; AE003529; AAF49557.1;
EMBL; AE003529; AAF49558.2;
PIR; A42091; A42091.
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                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                       PROSITE; PS0063; BROMODOMAIN_1; 1.

PROSITE; PS50014; BROMODOMAIN_2; 1.

Developmental protein; Transcription regulation; Nuclear protein;
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SIMILARITY: BELONGS TO THE SNE2/RAD54 HELICASE FAMILY.
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SM00487; DEXDC; 1.
SM00490; HELICC; 1
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903
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222
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                                                                                         DEGH BOX.

ASP/GLU-RICH (ACIDIC).

ASP/SLU-RICH (BASIC).

ASP/GLU-RICH (ACIDIC).

ASP/GLU-RICH (BCIDIC).
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BROMODOMAIN.
POLY-ASP.
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DYDRG------RTPSRHRSYERSRERERHRHRDNRRSPSLERSYKKEY
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Q1-MAR-2002 (Rel. 41, Last annotation
Ribonuclease III (EC 3.1.26.3) (RNase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 413:852-856(2001).
i- FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED OF RIBOSOMAL RNA PRECURSORS AND OF SOME MRNAS.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1;
PROSITE; PS50142; RNASE_3_2;
Hydrolaso, Nuclinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-LT2 / SGSC1412 / ATCC 70072
MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                      1161 YLFIHFPDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVGLRTKT-LAD 1219
                                                                                                                                                                                                                  1101 SPVLQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQLVATE 1160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00358; DSRM; SMART; SM00535; RIBOC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR001159; DS_RBD.
Interpro; IPR000999; RNase_3.
pfam; PF00035; dsrm; 1.
pfam; PF00636; Ribonuclease_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               StyGene; SG10695;
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                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase;
                                                             115
                                                                                                                         55
                                                                                                                                                                                       ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphomonoester.
SUBUNIT: ORCANIZED INTO A STRUCTURE (PROCESSOME) CONTAINING A NUMBER OF RNA-PROCESSING ENZYMES.
SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN.
SIMILARITY: CONTAINS 1 RNASE III DOMAIN.
                           DIPLYKTLQTVGPSHARTYTVAVYFKG--ERIGCGKGPSIQQAEMGAAMDALEK 1331
                                                             TVEALIGGVFLDSNIQTVEQLILNWYKTRLDEISPGDKQKDPKTRLQE-----YLQGRHL
                                                                                          LLESFIAALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLRTEGKEP 1279
                                                                                                                         {\tt ALYHRFPRVDEGDMSRMRATLVRGNTLAELAREFDLGECLRLGPGELKSGGFRRESILAD}
                                                                                                                                                                                     NPIV--INRLQRKLGYTFNHQELLQQALTHRSASSK-----HNERLEFLGDSILSFVIAN
PLPSYLVVQVRGEAHDQEFTIHCQVSGLSEPV-VGTGSSRRKAEQAAAEQALKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE008817:
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                                                                                                                                                                                                                                                     ; 69
                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                             208
57
73
217
226 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           Nuclease;
                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGSC1412 / ATCC 700720;
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224
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AT -> DP (IN REF. 1).
EQAL -> NSV (IN REF. 1).
; 5752C0113C0A055A CRC64;
                                                                                                                                                                                                                                                                                                                                                                              DRBM.
                                                                                                                                                                                                                                                                                                                                                                                             RNASE
                                                                                                                                                                                                                                                                                                                                                                                             RNA-binding;
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Search completed: October 9, 2002, 18:24:01
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Drosophila melanog
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AAR13995	ABG23699	ABG21919	AAU23180	ABB03068	AAB26153	AAR28150	AAG46150		AAG46152	AAW20772	ABB70063	AAM78694	ABG09877	AAE09769	ABB60977	ABB68526	ABG14000	ABG09876	ABB61946	AAG82282	AAW31852	AAW31855	ABG21932	AAY09366	ABB63064	AAM41045	ABB61362	AAM39259	ABB66989	AAW81354	ABG27250	ABG21040	ABB61598
extens	human	human	human enzv		ra NC-p65	C			Arabidopsis thalia	H. pylori cytoplas	phila		Novel human diagno	Drosophila melanog	Drosophila melanog			Novel human diagno	0		Mycobacterium tube	Mycobacterium tube	Novel human diagno	Staphylococcus aur	Drosophila melanog	Human polypeptide	Drosophila melanog	Human polypeptide	Ω	æ	Novel human diagno	Novel human diagno	Drosophila melanog

## ALIGNMENTS

RESULT 1 AAB92635

AAB92635;

AAB92635 standard; Protein;

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Ota T, ]
Ishii S,
                WPI; 2001-318749/34.
                                                                       29-JUL-1999; 99JP-0248036
27-AUG-1999; 99JP-0300253
11-JAN-2000; 2000JP-0118776
02-MAY-2000; 2000JP-0183767-
09-JUN-2000; 2000JP-0241899
                                                                                                                                                                                              Human; primer;
                                                                                                                                                                                                              Human protein sequence SEQ ID NO:10949
                                                                                                                           28-JUL-2000; 2000EP-0116126
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                                                                                                                                                                             Homo sapiens
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                                                        (HELI-) HELIX RES INST.
                               Isogai T, Nishikawa T,
, Sugiyama T, Wakamats
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                            detection; diagnosis; antisense therapy; gene therapy.
                                Wakamatsu
                               Hayashi K, S
A, Nagai K,
                                Saito K,
(, Otsuki
                                Η;
                                       Yamamoto
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Primer sets for synthesizing polynucleotides, particularly the 5602

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CC full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of cc the 5602 nucleotide sequences defined in the specification, where the colligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a polynucleotide which comprises the cc complementary strand of a polynucleotide which comprises a 5'-end cc complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence, where the cc oligonucleotide which comprises a 3'-end sequence, where the 5'-end sequence/3'-end sequence is selected from those defined in cc the 5'-end sequence/3'-end sequence is selected from those defined in cc the specification. The primer sets can be used in antisense therapy and cc in gene therapy. The primers are useful for synthesising polynucleotides, cc particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by ct the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cc AAH13633 to AAH18742 represent human cDNA sequences; and AAH13628 and cahH13633 to AAH18742 represent human cDNA sequences; and AAH13632 to AAH13632 crepresent oligonucleotides, all of which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventicuseful in developmental biology and in elucidating cell signalling a cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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11-JUL-2000;
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                                                                                                                                                                                                                                                          The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
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    PPPPPPPEEDLSPPGVGVPSHNYSSNESHSQ
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inappropriate expression of secreted proteins. (I) and complementary sequences may also be used as DNA probes in diagnostic assays (e.g. polymerase chain reactions (PCR)) to detect and quantitate the presence of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies may also be used as diagnostic agents for detecting the presence of (II) in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The
                                                                                                                                                                         encoding human secreted proteins (II). (I) and (II) are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) may be used it the prevention, treatment and diagnosis of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                  Rosen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1057
                                                                                                                                                                                                hyperproliferative disorder; neural disorder; immune system muscular disorder; reproductive disorder; gastrointestinal d pulmonary disorder; cardiovascular disorder; renal disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU21744;
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                                                           WO200155163-A1
                                                                                                                   Homo
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                                                                                                                                                                        neuroprotective;
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                                                                                                                                                                                                                                                                                  neoplastic disease associated polypeptide; cancer;
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28-JUN-2000;

28-JUN-2000;

29-JUN-2000;

20-JUL-2000;

11-JUL-2000;

14-JUL-2000;

14-JUL-2000;

14-AUG-2000;

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  14-SEP-2000;
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2000US-023143.
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Immunomodulatory; human immunodeficiency virus; HIV; anaemia;
rheumatoid arthritis; antiarteriosclerotic; cardiant; vascula;
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gastrointestinal disorders, pulmonary disorders, cardiovascular disorders and renal disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAUZ166-AAUZ1651 represent the novel human neoplastic disease associated polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the invention of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, also be useful for treating other disorders, reproductive disorders, immune system disorders, muscular disorders, reproductive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                    ATYRTAIVQNQHLAMLAKKLELDPFMLYAHGPDLCRESDLRHAMANCFEALIGAVYLEGS 1056
                                                                                                                                                                                       LEEAKQLFGRLLFNDPDLREVWLNYPLHPLQLQEPNTDRQLIETSPVLQKLTEFEEAIGV 1116
                                                                                                                                                                                                                                                                                              ATYRTAIVQNQHLAMLAKKLELDRFMLYAHGPDLCRESDLRHAMANCFEALIGAVYLEGS
                                      IFTHVRLLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQLVATEYLFIHFPDHHEGHLTL 1176
                                                                                                                                         LEEAKQLFGRLLFNDPDLREVWLNYPLHPLQLQEPNTDRQLIETSPVLQKLTEFEEAIGV 120
IFTHVRLLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQLVATEYLFIHFPDHHEGHLTL
                                                                                                                                                                                                                                                                                                                                                                                                                                           374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   26.1%;
nilarity 98.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ion relates to the isolation of novel human neoplastic polypeptides, and cDNA (AAS34767-AAS35050) and DNA for these polypeptides. The sequences of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1961; DB 22;
Pred. No. 5.3e-131;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 378;
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Best Local S
Matches 373
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                                                                                                                                                                                                                                                                                                cerebrovascular disorders (e.g. cardiac arrest, tachycardia, angina and thrombosis), infections caused by bacteria, viruses and fungi and ocular disorders (e.g. corneal infections). (I) and (II), agonists, antagonists and antibodies can also be used to promote wound healing, maintain organs before transplantation, and support cell culture of primary tissues. ANU2034-ANU20666 represent human secreted protein amino acid sequences, and related sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of similar nucleic acid sequences in samples, and so which patients may be in need of restorative therapy. (II) may also be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the secreted proteins. The anti-(II) antibodies and antagonists may also be used to down regulate expression and activity of (II). The anti-(II) antibodies may also be used as diagnostic agents for detecting the presence of (II) in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). The disorders include for example: immune/autoimmune diseases (e.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple colories.
                   1057,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and multiple sclerosis), cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of the breast or liver, Sezary Syndrome and Gaucher's disease, neurological diseases (e.g. Alzheimer's disease, Parkinson's disease and Charcot-Marie-Tooth disease), cardio-/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymerase chain reactions (PCR)) of similar nucleic acid sequences be in need of restorative therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombosis; wound healing.
                                                                                                                                                                                                                                      Sequence
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                                                                  <u>س</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to novel isolated nucleic acid molecules
                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                           ATYRTAIVQNQHLAMLAKKLELDPEMLYAHGPDLCRESDLRHAMANCFEALIGAVYLEGS 1056
                      LEEAKQLFGRLLFNDPDLREVWLNYPLHPLQLQEPNTDRQLIETSPVLQKLTEFEEAIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-451931/48
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Similarity
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                                                                                                                                                  Score 1956; DB 22;
Pred. No. 1.2e-130;
0; Mismatches 5;
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                                                                                                                                                                                            Length
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                  30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  hyperproliferative disorder; neural disorder; immune system disorder muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; rehal disorder;
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                                                                                                     14-JUL-2000;
26-JUL-2000;
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11-JUL-2000;
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19-MAY-2000;
                                                                                                                                                                                                                                 16-MAR-2000;
17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         neuroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; neoplastic disease associated polypeptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human neoplastic disease associated polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAU21580;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALEKYNFPQMAHQKRFIGRKYRQELKEMR 1356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VHTFMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLRTEGKEPDIPLYKTLQTVGPSHAR 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRSSLVNNRTQAKVÄBELGMQEYAITNDKTKRPVGLRTKTLADLLESFIÄALYTDKDLEY 1236
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                      2000US-0217487.

2000US-0218290.

2000US-0220963.

2000US-0220964.

2000US-0224518.

2000US-0224519.

2000US-0224519.

2000US-0225214.

2000US-0225214.

2000US-0225214.
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2000US-0205515.
2000US-0209467.
2000US-02114886.
2000US-02113135.
2000US-0216647.
2000US-0216880.
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2000US-0186350.
2000US-0189874.
2000US-0190076.
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                                                                                                                                                                                                                                                                                                               2001WO-US01358
                                                                                                                                                                                                                                                                                           2000US-0179065
                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic;
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14-SEP-2000
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14-SEP-2000
14-SEP-2000
14-SEP-2000
14-SEP-2000
21-SEP-2000
21-SEP-2000
25-SEP-2000
27-SEP-2000
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29-SEP-2000
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29-SEP-2000
29-SEP-2000
20-OCT-2000
02-OCT-2000
03-NOV-2000
04-NOV-2000
08-NOV-2000
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08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
12-SEP-2000;
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22-AUG-2000

22-AUG-2000

23-AUG-2000

30-AUG-2000

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01-SEP-2000

01-SEP-2000

01-SEP-2000

05-SEP-2000

05-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000
2000US-0225447
2000US-0225759
2000US-0225759
2000US-0226681
2000US-0226681
2000US-0226681
2000US-0229343
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2000US-0229513
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2000US-0234684
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2000US-02346477
2000US-0246477
2000US-0246523
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08-NOV-2000
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17-NOV-2000
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DB; AAS34779.
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2000US-0249215
2000US-0249217
2000US-0249218
2000US-0249244
2000US-0249244
2000US-0249264
2000US-0249264
2000US-0249297
2000US-0249297
2000US-0249300
2000US-0250160
2000US-0250160
2000US-0251988
2000US-0251988
2000US-0251479
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2000US-0251479
2000US-02514868
2000US-0251856
2000US-0251868
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2000US-0249208.

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2000US-0246609.
2000US-0246610.
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2000US-0246613.
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WPI; 200 N-PSDB;

Novel polypeptides and polynucleotides useful as diagnostic reagents diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, and for treating cancers, rheumatoid ç

Claim 11; SEQ ID ŏ 307; 687pp; English.

The present invention relates to the isolation of novel human neoplastic disease associated polypeptides, and cDNA (AAS34767-AAS35050) and DNA sequences encoding for these polypeptides. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of disorders involving neoplastic disease such as hyperproliferative disorders (e.g. leukaemia, bone cancer, bladder cancer, brain stem glioma, adult liver cancer, childhood cerebellar astrocytoma, or Hodgkin's lymphoma). The sequences of the invention may also be useful for treating other disorders such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders and renal disorders. The polynucleotide sequences of the invention are also useful in gene therapy. ANUZ1568-ANUZ1851 represent the novel human neoplastic disease associated polypeptides of the invention.

Note: The sequence data for this patent did not form part of the printed as first cont, but was obtained in electronic format directly from WIPO ftp.wipo.int/pub/published\_pct\_sequences

Sequence

Query Match

17.6%; Score 1320; DB 22; Length 263;

22;

Length

301;

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RESULT 7
AAAB632ET
AAAB632ET
AC AAB6
XX AAB6
XX AAB6
XX AAB6
XX AAB6
XX Can
DT 26-1
XX Can
DW Humm
KW Can
CX Home
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                                                              respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucle acids or anti-CAAP antibodies are useful for diagnosing and treating a condition characterised by expression of an abnormal amount of a protein
                                                                                                                                                                                                     AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014 represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
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                                                                                                                                                       represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the
                                                                                                                                                                                                                                                                                                                                         Example 1; Page 499; 799pp;
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                            represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively. AAB63222 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970 represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, nucleids or anti-CAAP antibodies are useful for diagnosing and treating condition characterised by expression of an abnormal amount of a protein condition characterised by expression of an abnormal amount of a protein condition characterised by expression of an abnormal amount of a protein condition characterised by expression of an abnormal amount of a protein condition characterised by expression of an abnormal amount of a protein can be conditioned by the condition characterised by expression of an abnormal amount of a protein can be conditioned by the cancel can be conditioned by expression of an abnormal amount of a protein can be conditioned by the cancel can be conditioned by expression of an abnormal amount of a protein can be called by the cancel can be cal
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                                                                                      represent nucleotide sequences encoding human breast, gastric and prostate cancer associated antigen precursors (CAAP) respectively AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
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                    represent human breast, gastric and prostate CAAP protein sequence respectively. CAAPs have cytostatic activity and can be used in the production of cancer vaccines. The human CAAP proteins, peptides, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
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Best Local
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                                                                                                                                                                                                                                                                                     Human; secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            condition characterised
                                                      New nucleic acids encoding human secreted proteins -cDNA libraries prepared from kidney, fetal kidney, duscle, muscle and heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                     AAY12224;
                                   Claim 34;
                                                                                                 N-PSDB;
                                                                                                                                 Duclert
                                                                                                                                                                            01-AUG-1997;
                                                                                                                                                                                                 31-JUL-1998;
                                                                                                                                                                                                                      11-FEB-1999
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             AAX40826 to
                                                                                                                                                    (GEST )
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                                                                                                1999-153784/13
DB; AAX41057.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIVQNOHLAMLAKKLELDPFMLYAHGPDLCRESDLRHAMANCFEALIGAVYLEGSLEEAK 1061
                                                                                                                                                                                                                                                                sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLFGRLLFNDPDLREVWLNYPLHPLQLQEPNTDRQLIETSPVLQKLTEFEEAIGVIFTHV
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                                                                                                                                                                                                                                                                                                                                                                EST secreted protein
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             AAX41093 represent 5'
                                                                                                                                Dumas Milne
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                                   599;
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                                   English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1122; DB 22;
Pred. No. 1.4e-71;
5; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO:
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RESULT 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 3' different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                             Claim 13; SEQ ID 4635; 71pp + CD-ROM; English
                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedure
                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Milne Edwards
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95.7%;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from oligo-dT 'primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                  genes from Drosophila
                                                                                                                                                                                               New isolated nucleic
                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                   Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231
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                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical.
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                                                                                                                                                                                                                                                                         (PEKE ) PE CORP NY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 KKAHPDRLHDELWYNDPGOMNDGPLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNNAGR 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88;
                                                                                                                                                                                                                      ABL05701
                                                                                                                                                                                                                                                                                                                                                                                                                                                           melanogaster polypeptide SEQ ID NO 11586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide;
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95.7%;
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                                                                                                                                                                                  detection reagent for detecting for elucidating cell signalling
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Pred. No. 1.2e-27;
                                                                                                                                                                                                                                                   Myers
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insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from

from

WIPO

(ABB57737-ABB72072).

at ftp.wipo.int/pub/published\_pct\_sequences

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of

invention

and S Disclosure; SEQ

ID NO 11586;

21pp + Sequence Listing; English

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ABG21040
ID ABG211
XX ABG21
XX HOVel
XX Human
KW Human
KW Hood
XX Homo
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                                    Human; chromosome mapping; gene mapping; gene therapy; forensic food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                            Novel human diagnostic protein #21031.
                                                                                                                                  18-FEB-2002
                                                                                                                                                                      ABG21040;
     Homo sapiens
                                                                                                                                                                                                       ABG21040 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 RPASPKVEPP-----PPAPPGVESPPGPQPPASPRFDPPPPHTIEPPPPPAPPTLVPPP 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83 PPMPPSAQGPLPPCP--IRPPFPNHQMRHPFPVPPCFPPMPPPMPCPN--NPPVPGAP-- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 RPSAPSFRPQNLRLLHPQQPPVQYQYEPPSAPSTTFSNSPAPNFL-----PPRPDFVPFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEEEE----LLKPVWIRCTHSENYYSSDPMDQVGDS----TVVGTSRLRDLYDKFEEELGSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KDHDRGRDRDRNKSNTSGSAENKAIHDDHSESKEKYKQRRGSDSNDEGKPPSSGGPAKNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSSSSKHSSSNSSSSKHKSSSSKNDKSSSSSSSRSNRESSSSKRSGTTSSSRHESSSHKK
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                                                                                                                                                                                                                                                                                                                                                                      -----PQDADKPATPVPISNEQSDEFSADF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEKAKAARPPWEPPKTKLDEDLESSSESECESDEDSTCSSSSD-----SEVFDVIAEIK 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----EYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSPSREKKRAR 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRYRSDYDRGR-TPSRHRSYERSRERERERHRHRDNRRSPSLER-----SYKK 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RRSTDRDRSRDKEKEKDRRHHRHSDDKH----RRRSTDRDRDRSRDKSHSKHS
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Pred. No. 3.1e-15;
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                                                                                                                                                                                                                                                                                                                                  671
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Note: The sequence data for this patent did not appear in the printed cast for the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS85227
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228
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                                                                                                                                                                                                                                                                                                                                                                    15 GRGCPRGR-----GGHGARPSAPSFRPQNLRLLHPQQPPVQYQYEPPSAPSTTFSNSP
                                                                                                                                                                                                                                                                                APNELPPRPDFVPFP------PPMP------PSAQ---GPLPPCPIRPPFPNHQMR 108
                                                                                                                                                                                                                                                                                                                                GRG--RGRFPGAVPGGDRFPGPAGPGGPP------PPFPAGQTPPRPPLGSFQGPP 250
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                                    RNRAISSSAISRAVSDASAGVDYGSAIETLVTAISLIKTIPKYP----ADDRCTKFLISS
                                                                        N----PSSFLPSANNSSSPH-----
                                                                                                                                                                                                                     HPFPVPPCFPPMPPPMPCPNNP-----
                                                                                                                                                                                                                                                         GPPGPPPPGQVLPPPLAGPPNRGDRPPPPVLFPGQPFGQPPLGPLPPGP-PPPVPGYG-P 308
                                                                                                           PPTNSGMPTSDSRGPPPTDP----YGRPPPYDRGDYGPPGREMDTARTPLSEAEFEEIMN
                                                                                                                                               PPSMPHPP-----PPPVMPQQVNYQYPPGYSHHNFPPP-----SFNSFQN 187
                                                                                                                                                                                  PPGPPPPQQGPPPPPGPFPPRPTGSNLGHPLTLAPPSASFPGPPPGAPPPSPHVNPAFFP 368
-HRHRDHSHGRGERHRSLDRRERGRSPDRRRQDSRYRSDYDRGRTPSRHRSYERSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  560 AA;
                                                                                                                                                                                                                                                                                                                                                                                                       4.1%; Score 311; DB 22;
29.5%; Pred. No. 1.4e-13;
tive 22; Mismatches 131
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-----PVPGA-PPGQGTFPFMMP 147

227 424 131;

120;

Gaps

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Length 560 Indels

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Best Local
                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                specification,
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                                                                                             te: The sequence data for this patent did not appear in the ecification, but was obtained in electronic format directly ftp.wipo.int/pub/published_pct_sequences.
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supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW81354 standard;
                                                                                                                                                         New isolated nucleic acid encoding rnc protein of Streptococcus pneumoniae - and related vectors, transformants, antibodies, proteins, and antagonists, for treatment, prevention and diagnos
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW81354;
                                                                                                                              Claim 12; Page 6; 22pp; English.
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protein of the invention. Cells containing the DNA are used to express rnc which is useful therapeutically; to screen for compounds that interact with, and activate or inhibit, it (potential antibacterial agents) and to generate antibodies (Ab) (including as vaccines to provide a protective response). The protein and its agonists are used to treat conditions where rnc polypeptide is required and the antagonists where rnc polypeptide needs to be inhibited, particularly a wide range of infections caused by S. pneumoniae, most particularly meningitis. The rnc protein also inhibit adhesion of bacteria to extracellular matrix

This sequence is the Streptococcus pneumoniae ribonuclease III (rnc)

proteins, in-dwelling devices and wound with expression of rnc are diagnosed: (a

nd surfaces. Diseases associated (a) by analysing a sample for

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Matches 75; Conservative
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                                                                                                                                                                                                                                                           presence of the protein; or (b) by detecting nucleic acid encoding the protein. Ab are useful as antibacterial agents; to isolate or identify rnc-expressing clones and for affinity purification. Fragments of the DNA are useful as probes or primers to isolate full-length or related sequences; to screen for drugs, and to diagnose or stage infections, also for genotyping and serotyping of infective agents (e.g. by detecting
                                                                                1224 FIAALYTDKDLEYYHTFMNVCFFPRLK--EFILNQDWNDPKSQLQQCCLTLRTEGKEPDI 1281
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                                                             176 AIRYQVISETGPAHDKVFDVEVLVEGKSIGQGQGRSKKLAEQEAAKNAVEK 226
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US-08-574-959A-7
US-09-357-014-7
US-09-357-014-7
US-09-323-735-4
US-08-818-111-113
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US-08-818-111-13
US-08-818-111-138
US-09-256-556-143
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US-09-234-613-47
US-09-234-613-47
US-09-234-633-6
US-08-899-595-3
US-08-899-595-3
US-08-899-595-3
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US-09-213-010-2
US-08-965-087-2
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Patent No. 5202236
Sequence 3, Appli
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Sequence 6, Appli
Sequence 2, Appli
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US-08-247-31C-2 US-08-290-731C-2 US-08-290-731C-6 US-08-290-731C-6 US-08-290-731C-6 US-08-217-536-2 PCT-US95-04682-2 US-09-316-952-2 US-09-316-952-2 US-09-316-952-2 US-09-316-952-2 US-08-211-38-2 US-08-211-38-2 US-08-211-38-6 PCT-US95-03236-21 US-09-150-4608-6 PCT-US95-03236-21 US-09-200-41-5 US-09-200-731C-4 US-09-303-064-54

## ALIGNMENTS

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RESULT 1
US-08-869-674-2
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                                                                         Query Match
Best Local 9
                                                        Matches
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APPLICANT: Lonetto, Michael A.
APPLICANT: Rosenberg, Martin
APPLICANT: ROSENBERG, MOVEL COMPOUNDS
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                     NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: GM10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version
1108 TEFEEAIGVIFTHVRLLARAFTLRTVGFNH--LTLGHNQRMEFLGDSIMQLVATEVLFIH 1165
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APPLICATION NUMBER: US/08/869,674
FILING DATE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3,
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
CITY: La
STATE: N
COUNTRY:
                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1166
1108 TEFEEAIGVIFTHVRLLARAFTLRTVGFNH--LTLGHNQRMEFLGDSIMQLVATEYLFIH 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bloom, Allen REGISTRATION NUMBER: 29,135 REFERENCE/DOCKET NUMBER: GM
                                               66
                                                                                                                                                                         Local Similarity
nes 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 609-520-3259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FPDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVGLRTK--TLADLLES 1223
                                                                                                           TVLKNHFAIEFADKNLLETAFTHTSYANEHRLLKISHNERLEFLGDAVLQLLISEYLYKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLGALLLDKDVAKVKEFIYQVMIPKVEAGEFEMITDY---KTHLQE---LLQVNG---DV 175
                                             YPKKPEGDLSKLRAMIVREESLAGFARDCQFDQF-IKLGKGEEKSGGRNRDTILGDAFEA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PL-YKTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALEK 1331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YPKKPEGDLSKLRAMIVREESLAGFARDCQFDQF-IKLGKGEEKSGGRNRDTILGDAFEA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVGLRTK--TLADLLES 1223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TVLKNHFAIEFADKNLLETAFTHTSYANEHRLLKISHNERLEFLGDAVLQLLISEYLYKK
                                                                                                                                                                                                                                                                                   amino acid
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ROSENDERG, MARTL...
ROYEL COMPOUNDS
                                                                                                                                                                                                                                                                                                232 amino acids
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                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                    ss: single
linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diskette
                                                                                                                                                                      3.7%; Score 277.5; DB 4; 32.5%; Pred. No. 3.6e-14; 47: Mismatches 92;
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                                                                                                                                                                                                     Length 232;
                                                                                                                                                                         Indels
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US-08-965-087-2
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Best Local Similarity 3v...
Thes 75; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,
                                                                                                                                                                    1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosenberg, Martin
APPLICANT: Warren, Richard L
TITLE OF INVENTION: NOVEL RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1282 PL-YKTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALEK 1331
                     1266
                                                                                                                                                                                                                                           1092 NTDRQLIETSPVLQKLTEFEEAIGVIFTHVRLLARAFTLRTV--GFNHLTLGHNQRMEFL 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                          1210 VGLRTK--TLADLLESFIAALYTDKDLEYVHTFMNVCFFPRLKEFILNQDWN--DPKSQL 1265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125
                                                         121
                                                                                                                                62
                                                                                                                                                                                                       11 NRFRKRFDT-----KMTE----LGFTYQNIDLYQQAFSHSSFINDFNMNRLDHNERLEFL 61
                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: li
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OPERATING SYSTEM:
SOFTWARE: FastSEC
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                                                                                                                                                                                                                                                                                                                                                                                                                TYPE:
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QQCCLTLRTEGKEPDIPLYKTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAA 1325
                                                                                                                                                                  GDSIMQLVATEYLFIHFPDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRP 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLGALLLDKDVAKVKEFIYQVMIPKVEAGEFEMITDY---KTHLQE---LLQVNG---DV
                                                       TGGRTRPSLISDAFEAFIGALYLDQGLDIVWKFAEKVIFPHVEQ----NELLGVVDFKTQF 177
                                                                                                                              GDAVLELTYSRYLFDKHPNLPEGNLTKMRATIVCEPSLVIFANKIGLNEMILLG-KGEEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19103
                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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4000 Bell Atlantic Tower,
                                                                                                                                                                                                                                                                                                                                                                                                                               243 amino acids
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Marra, Andrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215-994-2222
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                                                                                                                                                                                                                                                                                               3.6%;
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                                                                                                                                                                                                                                                                                  55; Mismatches
                                                                                                                                                                                                                                                                              Score 267; DB 4; repred. No. 2.6e-13; repred. No. 2.6e-23; representations 92;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1717 Arch Stre
                                                                                                                                                                                                                                                                                                                  Length 243;
                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                  Gaps
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Sequence 634227.

Patent No. 634227.

GENERAL INFORMATION:

APPLICANT: PLOWMAN, Gregory

APPLICANT: Peles, Eior

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT

OF INVENTION: OF ALP RELATED DISORDERS
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5202236-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; APPLICANT: MAUGH, SUSAN L.; MCCANDLISS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5202236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN
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                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG, IN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 25-MAY-1990
APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24 NOV-1986
APPLICATION NUMBER: 650,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173
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                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54
                                                                                                               COUNTRY: U.S.A. ZIP: 90071-2066
                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/07/528,762 FILING DATE: 25-MAY-1990
SOFTWARE:
                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P----PTYKAKP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPSYPPTYKAKPSYPPTYKAKPTYKIKPTYPSTYKAKPTNPSTYKAKPSYPPTYKAKPSY 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --QYPPGY-SHHNFPP-----PSFNSFQNNPSSFLPSANNSSS------PHFRHLPPY 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPAPPAPAFAPALAPAPPNPN--PQSPPSPPSPPTP-PPTPPSPPAP-----PSP 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESAYKQ 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPSPPNPPPSP-PPSPPFPPAPPPSPPFPPTYKAKPTYKAKPTNPSTYKAKPSYPPTYKA 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                   Los Angeles
: California
                                                                                                                                                                                       Suite 4700
                                                                                                                                                                                                       E: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
FastSEQ
             IBM Compatible
SYSTEM: IBM P.C. DOS 5.0
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31.8%;
for Windows 2.0
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Pred. No. 7e-10;
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                                                                                                                                           520236-37
520236-37
;Patent No. 5202236
; Patent No. 5202236
; Patent No. 5202236
; APPLICANT: MAUGH, KATHY J.; ANDERSON, DAVID M.; STRAUSBERG,
; SUSAN L.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID
; SUSAN I.; MCCANDLISS, RUSS; WEI, TENA; FILPULA, DAVID
; TITLE OF INVENTION: METHOD OF PRODUCING BIOADHESIVE
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                                                                                                                                                                                                                                                                                   RESULT 6
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Best Local Similarity 29.8
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 67-3510 INFORMATION FOR SEQ ID NO:
                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/0
FILING DATE: June 12, 19
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            890 LSPYCPPLVATQAPLPGTA---ADFW 912
                                                                                                                                                                                                                                                                                                                                                                                                                    840 QEHDARGRSIAIARCYSL-----KNRHQDVMPYDSNR----VVLRSGKDDYINASCVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               629 LLPPQSPYP--YAPQPGVLGQPPP-PLHTQ--LYPGPAQDPLPAHSGALPFPSPGPPQPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       574 HHFSSGIPTGFPAPRIGPQPQPHPQPHPSQAFGPQ-----PPQQPLPLQHPHLFPPQAPG 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                            271
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STRANDEDNESS: si
TOPOLOGY: linear
               APPLICATION NUMBER: 82,456
FILING DATE: 07-AUG-1987
APPLICATION NUMBER: 933,945
FILING DATE: 24-NOV-1986
                                                                                         APPLICATION NUMBER: US/07/528,762 FILING DATE: 25-MAY-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME:
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APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----RGRTPSRHRSYERSRERERERHRHRD-----NRRSPSLERSYKKEYKRSGRSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEGRRPQALRLIERDPYEH-----PERLRQLQQELEAFRGQLGDVGALDTVWRELQDA 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APSERRSPERLKHYDDHRHRDHSHGRGERHRSLDRR----ERGRSPDRRRQDSRYRSDYD- 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --PPAAE----PPPCLR-----RGAAAADLLSSSPESQHGGTQSPGGGQPLLQPTKVDA 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QYPPGYSHHNFPPPSFNSFQNNPSSFLPSANNSSSPHFRH------LPPYPLPK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPPLAYGPAPSTRPMGPQAAPLTIRGPSSAGQSTPSPHLVPSPA-PSPGPGPVPPR----
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                                                                                                                                                                                                                                                                                                                                                                                LSVVPEPAGCT-PELPGEIIKNTDSW 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1274 amino acids
NUMBER: 650,128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.0%; Score 226; DB 4; 29.8%; Pred. No. 4.8e-09;
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US-09-041-886-23
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                                                                                                                                                             ; MOLECULE TYPE: protein US-09-041-886-23
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                                                                    Query Match 2.9%; Score 220.5; DB 4; Best Local Similarity 21.5%; Pred. No. 1.2e-08; Matches 125; Conservative 29; Mismatches 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.0%; Score 225.5; DB 6; Best Local Similarity 31.2%; Pred. No. 7.5e-10; Matches 64; Conservative 13; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bredesen, Papplicant: Rabizadeh, Sharroz
APPLICANT: Rabizadeh, Sharroz
TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1185 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2626
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157 PSYPPTYKAKPSYP----PTYKAKP 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 TYKAKP-SYPPTYKAKPSYPPTYKAKPTYKIKPTY-----PSTYKAKPTNPSTY--KAK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198 NSSSPHFRHLPPYPLPKAPSERRSP 222
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14 PGRGC------PRGRG-GHGARPSAPSFRPQNLRLLH-------PQQPPVQYQYEP 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54 PPNPPPSPPPSPPPP-----PAPPPSPPFPPTYKAKPTYKAKPTNPSTYKAKPSYPP 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 PSAPSFRPQNLRLLHPQQPPVQYQYEPPSAPSTTFSNSPAPNFLPPRPDFVPFPPPMPPS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Campbell & Flores LLP 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Version #1.25
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                                                                      Indels 279;
                                                                                                             Length 1185;
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                                                                    Gaps
                                                                      28;
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			RE US	ОУ	Db	γ	Оу	Qy Db	Ор	Db CF	О	Db ?	Q (	ДУ	) Db
CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/812,233 ETLING DATE: 19-DEC-1991 ATTORNEY/AGENT INFORMATION: NAME: Seay, Nicholas J REGISTRATION NUMBER: 27,386 REFERENCE/DOCKET NUMBER: 1122990831 TELECOMMUNICATION INFORMATION: TELEPHONE: 608-251-5000	CUUNIKI: USA ZIP: 53701-2113 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/217,327 FILING DATE:	APPLICANT: John, Maliyakal E APPLICANT: Barton, Kenneth A TITLE OF INVENTION: Immobilized Proteins in Cotton Fiber NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSEE: Quarles and Brady STREET: P.O. Box 2113 CITY: Madison STATE: WI	RESULT 8 US-08-217-327-6 US-08-217327-6 ; Sequence 6, Application US/08217327 ; Patent NO. 5474925 ; GEMERAL INFORMATION:	316 RSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSP 356	EGSKLAKKRADLVEKVRREAEQRAREEKEREREKEREF	273RTPSRHRSYERSRERERHRHRDNRRSPSLERSYKKEYKRSG 315	235 DHSHGRGERHRSLDRRERGRSPDRRRQDSRYRSDYDRG 272	186 QNNPSSF	156NSF 185		PPPPGAFPHPLEGGSSHAHPYAMSPS		AOGPLPPCPIRP-PFPNHOMRNHOMR	56 PSAPSTTESNSPAPNELPPRDEVPEPPMPPS	PGLGAQPLPGHLPSPYAMGQGMGGLPPGPEKGPTLAPSPHSLPPASSSAPAPPMRFPYSS

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US-08-574-959A-9
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US-08-574-959A-9
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Best Local Similarity
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                                                                                                            NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
                                                                                      TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                APPLICATION NUMBER: US/O
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREFOR
                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289 PPPKHH 294
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                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94 ---PPCPIRPPFPNHQMRHPFPVPPC-----FPPMPPPMPCP-----NNPPVP----- 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 PPPPYHYESPPPPKHSPPPPTPVYKYKSPPPPMHSPPPPYHFESPPPPKHSPPPPTPVYK 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 PPVQYQYE-----PPSAPSTTFSNSPAPNFLPPRPDFVPFPPPMPPSAQGPL---- 93
                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                        TOPOLOGY:
                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNFPPPSFNSFQNNPSSFLPSANNSSSPHFRHLPPYPLP------KAPSERRSP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YKSPPPP----EHSPPPPTPVYKYKSPPPPMHSPPPPTPVYKYKSPPPPMHSPPPPVYSP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GAPPGQGTFPFWMPPPSMP-----HPPPPPPVMPQQV-NYQY----PPGYSH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEHHYKYKYKSPPPPTPVYKYKSPPPPTPVYKYKSPPPPKHSPAPVHHYKYKSPPPPTPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                            02109-1875
                                                    amino acid
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                                                                      905 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: LAHIVE & COCKFIELD 60 State Street, Suite 510
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                                      linear
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19-DEC-95
                  protein
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RESULT 10
US-09-357-014-9
US-09-357-014-9
IS equence 9, Application US/09357014
Patent No. 6291645
Patent No. 6291645

GENERAL INFORMATION:
APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
AND USES THEREFOR
USES THEREFOR
OUTTY: Boston
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/574,959

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; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-357-014-9
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                                                                                                                                                                                            US-08-574-959A-7
                                                                                                                                                 Sequence 7, Application US/08574959A Patent No. 5962224
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                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 9:
APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi APPLICANT: and Jack L. Strominger TITLE oF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDE: TITLE OF INVENTION: AND USES THEREFOR NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169
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                                                                                                                                                                                                                                                                                842 EETEDGSDKVQ-----PPPETPAEEEMETETEAEALQEKEQDDTAAMLAD 886
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 905 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: MANDISON NUMBER: 36,207
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPSGATPP-PIAPTGP---PTASPPVPAKEEPEELPAAPGPLPPPPPPPPPPVPGPV----
                                                                                                                                                                                                                                                                                                        EELGSRQEKAKAARPPWEPPKTKLDEDLESSSESEC--ESDEDSTCSSSSD 498
                                                                                                                                                                                                                                                                                                                                                                                                         DKNEEEEEELLKPVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDK------FE 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----XLPPPQLVP-EGTPGGGGPPALEEDLTVININSSDE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPGYSHHNFPPPSFNSFQNNPSSFLPSA-----NNSSSPHFRHLPPYPLPKAPSERR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPCPNNPPVPGAPPGQGTFPFMMPP--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -PPTIPPDETFGGRVP----RPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPP 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPPPMPPSAQ--GPLPPCPIRPPFPNHQMRHPFP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRSYERSRERERHRHRDNRRSPSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEI 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPERLKHYDDHRHRDHSHGRGERHRSLDRRERGRS----PDRRRQDSRYRSDYDRGRTPSR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAGPMPSAGPVPSEPWTSTTANLLGLLSRPSVCPPRLLPGPENHRAGSNEDPILAPSGTP 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SA-----PSTTFSNSPA------PNFLPPR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IKNTDSWAPPLEIVNHRSPSREKKRARWEEEKDRWSDNQSSGKDKNYTSIKEKEPEETMP 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEEGELE-EEEEEEDEEEEELEEVEDLEFGTAG-----GEVEEGAPPPPTLPPAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative 58; Mismatches 212; Indels 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                -PPPESPPKVQPEPEPEGLLLEVEEPGTE-EERGADTAPTL----APEALP
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Pred. No. 1.8e-08;
                                                                                                                                                                                                                                                                                                                                                                 ----GESPAAGPPP-QELVEEEPSXPPTLLE
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                                                                 RELATED POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----PSMPHPPPPPVMPQQVNYQY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---- VPPCFPPMPPP 123
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Best Local Similarity
Matches 125; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/574,959A
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: DF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 60 St
CITY: Boston
STATE: Massac
                                                                                                                                                                                               338
                                                                                                                                                                                                                                    942
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                                                                                                                                                                                                                                                                                                                                                      221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 MPCPNNPPVPGAPPGQGTFPFMMPP------PSMPHPPPPPVMPQQVNYQY 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 FPPPMPPSAQ--GPLPPCPIRPPFPNHQMRHPFP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 σ
                                                                                                                  DKNEEEEEELLKPVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDK-----FE 449
                                                                                                                                                                                                                                    ----EEEGELE-EEEEEEDEEEEEELEEVEDLEFGTAG-----GEVEEGAPPPPTLPPAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -PPTIPPDETFGGRVP----RPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SA-----PSTTFSNSPA-----PNFLPPR-----
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EETEDGSDKVQ----
                                    EELGSRQEKAKAARPPWEPPKTKLDEDLESSSESEC--ESDEDSTCSSSSD
                                                                                                                                                      -----pppesppkvqpepepepgllleveepgte-eergadtaptl-----apealp
                                                                                                                                                                                             IKNTDSWAPPLEIVNHRSPSREKKRARWEEEKDRWSDNQSSGKDKNYTSIKEKEPEETMP 397
                                                                                                                                                                                                                                                                        HRSYERSRERERHRHRDNRRSPSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEI 337
                                                                                                                                                                                                                                                                                                               ----XLPPPQLVP-EGTPGGGGPPALEEDLTVININSSDE----
                                                                                                                                                                                                                                                                                                                                                                                                                               PPGYSHHNFPPPSFNSFQNNPSSFLPSA-----NNSSSPHFRHLPPYPLPKAPSERR 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPSGATPP-PIAPTGP---PTASPPVPAKEEPEELPAAPGPLPPPPPPPPPPVPGPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             {\tt SAGPMPSAGPVPSEPWTSTTANLLGLLSRPSVCPPRLLPGPENHRAGSNEDPILAPSGTP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H: 1135 amino acids
amino acid
DGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: LAHIVE & COCKFIELD 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (617)227-5941
(617)0: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
---pppetpaeemeteteaealQekeQDDTaamLaD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.9%; Score 216; DB 2; J
21.2%; Pred. No. 2.5e-08;
htive 58; Mismatches 212;
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                                                                           -GESPAAGPPP-QELVEEEPSXPPTLLE
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RESULT 12
US-09-357-014-7
; Sequence 7, Application
; Patent No. 6291645
; Patent No. FORMATION:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ
US-09-357-014-7
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                                                                                                                                                                    798
                                                                                                                                                                                                              124
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                                                                                                                                                                                                                                                                                                                                           683
                                                                                                                                                                                                                                                                                                                                                                                                                        624 TCAALT-HPRVPPLQPMGPTCPTPAPVPLLRPHRPSGPHRSILRAPCPQWAPCPQQAPCP
                                                                                                                                                                                                                                                                                        81 FPPPMPPSAQ--GPLPPCPIRPPFPNHQMRHPFP------VPPCFPPMPPP 123
                                                                                                                                                                                                                                                                                                                                                                              57 SA------PSTTFSNSPA------PNFLPPR------PDFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 TCHRMSFHP------GRGCPRGRGGHGARPSAPSFRPQN-LRLLHPQQPPVQYQYEPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 2.9%;
Local Similarity 21.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPERENCE/DOCKET NUMBER: DFN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/574,959 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jackyoon Shin, Insil Joung, Ratna K. Vadlamudi and Jack L. Strominger TITLE OF INVENTION: P62 POLYPEPTIDES, RELATED POLYPEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                   SPERLKHYDDHRHRDHSHGRGERHRSLDRRERGRS---PDRRRQDSRYRSDYDRGRTPSR 277
EGEEEEEEEEEEEEEEEEEEEEEEEDFEEEEEYFEEEEEEEFEEFE-----
                                                                                                                                                                                                        MPCPNNPPVPGAPPGQGTFPFMMPP-----
                                                                                                                                                                                                                                                  -PPTIPPDETFGGRVP----RPAFVHYDKEEASDVEISLESDSDDSVVIVPEGLPPLPPP
                                                                                                                                                                                                                                                                                                                                    SAGPMPSAGPVPSEPWTSTTANLLGLLSRPSVCPPRLLPGPENHRAGSNEDPILAPSGTP
                                                                                                                     PPGYSHHNFPPPSFNSFQNNPSSFLPSA-----NNSSSPHFRHLPPYPLPKAPSERR 220
                                                                                                                                                                PPSGATPP-PIAPTGP---PTASPPVPAKEEPEELPAAPGPLPPPPPPPPPPPVPGPV----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09357014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1135 amino acids
                                                                             ---XLPPPQLVP-EGTPGGGGPPALEEDLTVININSSDE
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%; Pred. No. 2.5e-08;
58; Mismatches 212; Indels 196; Gaps
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밁
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US-09-080-897-4
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                                                                                                                                        Query Match
Best Local Similarity 32.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4,
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                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORIEY / AGENT INFORMATION:
ATORIEY OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (650) 343-43.
INFORMATION FOR SEQ ID NO:
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APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1072 EETEDGSDKVQ------PPPETPAEEEMETETEAEALQEKEQDDTAAMLAD 1116
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620 GACIPPPPQLPGSAAIPPPPPLPGVASIPPPPPLPGATAIPPPPPPLPGATAIP----PPPP 676
                                   114 PPCFPP------MPPPMPCPN-----NPPVPGAP------PGQGTFPFMMPPPS 150
                                                                         562 APSYSSSAAVPP--APPLEGDSGTVIPPPPPPPPPPPLPGGVVPPSPPLPPGTCIPPPPPLPG 619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: HILLSBOROUGH
                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
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                                                                                                                 APSTTFSNSPAPNFLPPRP----DFVPFPPPMPPSAQGPLPPCPIRPPFPNHQMRHPFPV 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EELGSRQEKAKAARPPWEPPKTKLDEDLESSSESEC--ESDEDSTCSSSSD 498
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                                                                                                                                                                                                                                                                                                                                        1255 amino acids
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Welcsh, Piri L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    King, Mary-Claire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee, Ming
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                                                                                                                                                                                                                                                                                                                                                                                                     343-4342
                                                                                                                                                     2.7%; Score 203; DB 2; I
32.1%; Pred. No. 3.1e-07;
11. Mismatches 72;
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                                                                                                                                                                                               Length 1255;
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US-08-899-595-1
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                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 25-MAR-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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677 LPGGTGIPPPPPLPGSVGVPPPPPLPGGPGLPPP-----PPPFPGAPGIPPPPPGM 728
                                                                                                                                                    562 APSVSSSAAVPP--APPLPGDSGTVIPPPPPPPPPPLPGGVVPPSPPLPPGTCIPPPPPLPG 619
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                                                                        620 GACIPPPPQLPGSAAIPPPPPLPGVASIPPPPPLPGATAIPPPPPLPGATAIP---PPPP 676
                                                                                                           114 PPCFPP-----MPPPMPCPN-----NPPVPGAP------PGQGTFPFMMPPPS 150
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                                                                                                                                                                                                                                            Local
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FILING DATE: 26-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                        58 APSTTESNSPAPNELPPRP----DEVPEPPPMPPSAQGELPPCPIRPPEPNHQMRHPEPV 113
                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP 9-90170 FILING DATE: 25-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/899,595 FILING DATE: 24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                 MPH----PPPPPVMPQQVNYQYPPGY-SHHNFPPPSFNSFQNNPSSFLPSANNSSSPHFR 205
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                                                                                                                                                                                                                               63;
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                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.C.
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                               1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                        : (202)672-5300
(202)672-5399
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                         2.7%; Score 203; DB 3; L
32.1%; Pred. No. 3.1e-07;
71. Mismatches 72;
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Best Local Similarity
Thes 63; Conserve
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US-09-323-735-4
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GENERAL INFORMATION:
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INFORMATION FOR SEQ
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REFERENCE/DOCKET NUMBER: UW
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Modulators of Actin NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                     206 HLPPYP----LPKAP 216
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                                                                                                             MPH----PPPPPVMPQQVNYQYPPGY-SHHNFPPPSFNSFQNNPSSFLPSANNSSSPHFR 205
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Pred. No. 3.1e-07;
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US-09-547-599C-3281
US-09-915-537-130915
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RESULT 1 US-09-629-469A-10949; Sequence 10949; Ap GENERAL INFORMATIO ; APPLICANT: OTA, T ; APPLICANT: NISHI ; APPLICANT: HAYAS ; APPLICANT: YAWAM ; APPLICANT: TSUAM ; APPLICANT: SATO ; APPLICA		45	Δ Δ Δ	42	41	40	39	37	36	35	34	ω ω	32	31	30	29	28	27
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10949 49, Application US/ RMATION: OTA, TOSHIO ISCCAI, TAKAO NISHIKAWA, TETSUO HAYASHI, KOJI SAITO, KAORU YAMAMOTO, JUNICHI ISHII, SHIZUKO		ω : ω :	ມ ເມ ມ ເມ			٠	ω ι 			3.4	3.4	3.4	3.4	3.4	3.4		3.5	•
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69A-10949 10949, Application US/09629469A NFORWATION: TY: OTA, TOSHIO TY: ISOGAI, TAKAO TY: NISHIKAWA, TETSUO TY: HAYASHI, KOJI TY: SAITO, KAORU TY: YAMAMOTO, JUNICHI TY: YAMAMOTO, JUNICHI TY: ISHII, SHIZUKO	ALIGNMENTS	-625	4	9-	US-09-935-625-8099	US-09-935-625-5343	US-09-935-625-900	US-09-791-537-130916	US-10-055-797-4	US-09-858-862-4	US-09-866-557A-4	US-10-179-131-5134	US-09-791-537-130365	PCT-US02-16676-9	PCT-US02-25485-2790	US-09-791-537-38286	6	US-09-935-625-9404
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; SEQ ID NO 10949
; LENOTH: 769
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-629-469A-10949
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TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FUI
FILLE REFERENCE: 084335/0123
CURRENT APPLICATION NUMBER: US/09/629,469A
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: JP 1999-248036
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 1999-300253
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR APPLICATION NUMBER: 60/159,590
PRIOR FILING DATE: 1999-10-18
                                                                                                Query Match 54.3%;
Best Local Similarity 99.5%;
Matches 765; Conservative
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PRIOR FILING DATE: 2000-02-17
NUMBER OF SED ID NOS: 19025
SOFTWARE: Patentin Ver. 2.1
                        606 MFAHAPLTNIPLCKVIRFNIDYTIHFIEEMMPENFCVKGLELFSLFLFRDILELVDWNLK 665
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Pred. No. 4e-185;
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APPLICANT: Brooksbank, Robert
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use of
FILE REFERENCE: WL-A-018199
CURRENT APPLICATION NUMBER: US/10/205,331
CURRENT FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: GB 0118354.0
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 117
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 116
LENGTH: 541
mvor. DDT
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                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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CURRENT APPLICATION NUMBER: US/99/764,882A
CURRENT ETLING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILLING DATE: 2000-01-31
PRIOR FILLING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/218,628
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILLING DATE: 2000-06-28
PRIOR FILLING DATE: 2000-06-28
PRIOR FILLING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR APPLICATION NUMBER: 60/220,963
PRIOR FILLING DATE: 2000-07-16
PRIOR FILLING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: 60/217,496
PRIOR APPLICATION NUMBER: 60/225,447
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Best Local S
Matches 537
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                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: PTZ15
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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APPLICATION FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNQDWNDPKSQLQQCCLTLRTEGKEPDIPLYKTLQTVGPSHARTYTVAVYFKGERIGCGK 1313
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              NUMBER:
2000-07-14
                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids, Proteins, and
                60/218,290
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2.8e-127;
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; PRIOR	2000-09-05 NUMBER: 60/236,		RIOR
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; PRIOR	: 2000-	OR FILING DATE OR APPLICATION	RIOR
; PRIOR	NUMBER	APPLIC	RIOR
; PRIOR	ON NUMBER: 60/229,287	APPLIC	RIOR
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PRIOR	: 2000-09-01		RIOR
; PRIOR	: 2000-09-25	FILING DAT	RIOR
; PRIOR	ON NUMBER: 60/234,997		TOR
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; PRIOR	TE: 2000-09-29 ON NUMBER: 60/251,856		TOR
; PRIOR	NUMBER:	R APPLIC	õ
; PRIOR	DN NUMBER: 60/225,268	APPLICATION	~IOR
; PRIOR	2000-11-01	FILING DATE	TOR
; PRIOR	2000-10-2 NUMBER: 60	APPLICATION	~IOR
; PRIOR	DN NUMBER: 60/241,785	APPLICATION	~ior
; PRIOR	DN NUMBER: 60/236,327	APPLICATION	RIOR
; PRIOR	ON NUMBER: 60/249,299	FILING DATE	CIOR
; PRIOR	: 2000-10-20	FILING DATE	TOR
; PRIOR	TE: 2000-07-26 DN NUMBER: 60/241,809	APPLICATION	CIOR
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; PRIOR	NUMBER: 6	APPLIC	TOR CIOR
; PRIOR	: 2000-09-29		CIOR
; PRIOR	: 2000-08-14		TOR
; PRIOR	TE: 2000-08-30 ON NUMBER: 60/224,518	OR APPLICATION	CIOR
PRIOR	NUMBER: 6	APPLIC.	ior ior
PRIOR	TE: 2000-09-21	OR FILING DATE:	CIOR S
; PRIOR	: 2000-09-21		CIOR
; PRIOR	TE: 2000-09-27	OR FILING DATE	TOR
; PRIOR	NUMBER: 6	APPLIC.	IOR
; PRIOR	DN NUMBER: 60/251,869	OR APPLICATION	TOR
PRIOR	: 2000-08-14		IOR
; PRIOR	DN NITMBER: 60/225.270	OR FILING DATE	TOR
PRIOR	NUMBER: 6	APPLICA	IOR
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; PRIOR	IE: 2000-07-07	OR APPLICATION OR FILING DATE	IOR
PRIOR	: 2000-08-22		IOR
; PRIOR	: 2000-08	OR FILING DATE	IOR
; PRIOR	NUMBER: 60/225,757	APPLICA	IOR
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OR REILING DATE: 2000-10-02
OR APPLICATION NUMBER: 60/237,037
OR FILLING DATE: 2000-10-02
OR APPLICATION NUMBER: 60/237,040
OR FILLING DATE: 2000-10-02
OR APPLICATION NUMBER: 60/249,960
OR FILLING DATE: 2000-10-13
OR APPLICATION NUMBER: 60/239,935
OR FILLING DATE: 2000-10-13
OR APPLICATION NUMBER: 60/244,78
OR APPLICATION NUMBER: 60/245,216
OR FILLING DATE: 2000-11-08
OR PILLING DATE: 2000-11-17
OR APPLICATION NUMBER: 60/249,216
OR APPLICATION NUMBER: 60/249,216
OR APPLICATION NUMBER: 60/225,759
OR FILLING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/225,759
OR FILLING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/225,759
OR APPLICATION NUMBER: 60/225,719
OR APPLICATION NUMBER: 60/235,836
OR FILLING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/235,836
OR FILLING DATE: 2000-09-27
OR APPLICATION NUMBER: 60/249,213
OR APPLICATION NUMBER: 60/249,214
OR APPLICATION NUMBER: 60/249,215
OR APPLICATION NUMBER: 60/249,216
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APPLICATION FILING DATE:

NUMBER:

60/231,414

2000-09-08

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US-10-103-313-471

Sequence 471, Application US/10103313

GENERAL INFORMATION:
APPLICAMT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, an
FILE REFERENCE: PJZ07C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
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APPLICATION NUMBER:
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APPLICATION NUMBER: 60/232,399
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APPLICATION NUMBER: 60/246,475
FILING DATE: 2000-11-08
APPLICATION NUMBER: 60/231,243
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APPLICATION NUMBER: 60/241,826
FILING DATE: 2000-10-20
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APPLICATION NUMBER: 60/241,808
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APPLICATION NUMBER: 60/232,401
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FILING DATE: 2000-09-14
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FILING DATE: 2000-09-14
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                                                                                                                                                                                                             WEREHQEREPDETEDIKK
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PRIOR FILING DATE: 2000-01-31
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PRIOR APPLICATION NUMBER: 60/220,963
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APPLICATION NUMBER: 60/226,868

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                            Prior Application removed - See File Wrapper or SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 307
                                                                                                                                                                                           Sequence 307, Application US/10103313 GENERAL INFORMATION:
                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ07C1
CURRENT APPLICATION NUMBER: US/10/103,313
CURRENT FILING DATE: 2002-03-12
NUMBER OF SEQ ID NOS: 653
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OR FILING DATE: 2000-10-20
OR APPLICATION NUMBER: 60/241,221
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OR APPLICATION NUMBER: 60/246,475
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Pred. No. 3.1e-85
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PRIOR APPLICATION NUMBER: US 08/905,279
PRIOR PILING DATE: 1997-08-01
PRIOR PPLICATION NUMBER: US 08/904,468
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,134
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
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SEQ ID NO 3281
LENGTH: 115
TYPE: PRT
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PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,135
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR APPLICATION NUMBER: US 08/905,051
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
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APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: Expressed Sequence Tags and
FILE REFERENCE: GEN-T119C1
CURRENT APPLICATION NUMBER: US/09/547,599C
CURRENT FILING DATE: 2000-04-11
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APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 3475
                                                          LOCATION: -23..-1
OTHER INFORMATION:
OTHER INFORMATION:
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FEATURE:
                    OTHER INFORMATION:
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NAME/KEY: SIGNAL
                                                                                                                                                                        OTHER INFORMATION: kidney
                                            FEATURE:
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Pred. No. 2.9e-55;
0; Mismatches 6;
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RESULT 9
US-09-791-537-62108
; Sequence 62108, Application US/09791537
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 130915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Blonomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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    APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE:
                                                                                           APPLICANT: Bionomix, Inc.
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Similarity 95.7%;
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2001-02-22
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Pred. No. 1.3e-16;
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SOFTWARE: Patentin version 3.0

SEQ ID NO 104336

LENGTH: 266

TYPE: PRT

ORGANISM: Bacillus subtilis

US-09-791-537-104336
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SOFTWARE: Patentin version 3
SEO ID NO 62108
LENGTH: 266
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Best Local
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APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
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CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
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Local Similarity 34.28;
les 83; Conservative
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                                       EPDIPLYKTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDA---LEKYNF 1334
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E ----
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                                                                                                                                                                                                                                                                                  VEQFKEFQERISVHFQNEKLLYQAFTHSSYVNEHRKKPYEDNERLEFLGDAVLELTISRF 76
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                                                                                           FKAFIGALYLDQGLEPVESFLKVYVFPKINDGAFPHVM-DFKSQLQE---YVQRDGKGSL
                                                                                                                                                                                      LFPKYPAMSEGDLTKLRAAIVCEPSLVSLAHELSFGDLVLLGKGEEMTGGRKRPALLADV 136
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-YKISNEKGPAHNREFEAIVSLKGEPLGVGNGRSKKEAEQHAAQEALAKLEKHHT
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34.6%; Pred. No. 2.5e-07;
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US-10-216-583-1603
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CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION UNMEER: 09/760,469
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-06-8
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,758
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,758
PRIOR FILING DATE: 2000-08-14
PRIOR FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1963
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1603
LENGTH: 480
TYPE: PRT
ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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Best Local (
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PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/218,290
PRIOR FILING DATE: 2000-07-14
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LOCATION: (330)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (189)
OTHER INFORMATION: Xaa equals any
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LOCATION: (183)
OTHER INFORMATION: Xaa equals any of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIOR APPLICATION NUMBER: 60/220,963
RIOR FILING DATE: 2000-07-26
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151 MPHPPP--PPVMPQQVNYQYPPGYSHHNFPPPSFNSFQNNPSSFLPSANNSSSP---HFR 205
                                                                           225 PPPPVPGYGPP-----PGPPPPQQGPPPPPGPFPPRPPGPLGPP-----LTLAPPPH 271
                                                                                                                                                                         167 SQFEMQSRKTTQSGQMXGEGKAXPPLAGPPNRGDRPPPP--VLFPGQPFGQPPLGPLPPG
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Local Similarity 27.2%;
hes 111; Conservative 3
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                                                                                                                         PLPPCP-IRPPEPNHQMRHPFPVPPCFPPMPPPMPCPNNPPVPGAPPGQGTFPFMMPPPS 150
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- 454	407 LLKPVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGS	0γ	
K 642	583 GRKHQRERRSPGRLSEEQDRVQNSKLLKRTSVPDTDKRKQLPEKLLEVGRVEHYKEQERK	DЬ	
E 406	RARWEEEKDRWSDNQSSGKDKNYTSIKEKEPEETMPDKNEEEEE	Qy	
R 358   R 582	300 SPSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSPS- 	Qy Db	
R 299 R 558	240 RGERHRSLDRRERGRSPDRRRQDSRYRSDYDRGRTPSRHRSYERSRERERERHRHRDNRR	Qу	
	191 SFLPSANNSSSPHFRHLPPYPLPKAPSERRSPERLKHYDDHRHRDHSH	Qу	
s 190 1 S 459	138 GQGTFPFMMPPPSMPHPPPPPVMPQQVNYQYPPGYSHHNFPPPSFNSFQNNPS :	Qy	
P 137     414	105 HQMPGAPP   105 HQMPGAPP   105 HQMPGAPP   107 HQ	Qy Db	
N 104	55 PPSAPSTTFSNSPAPNFLPPRPDEVPFPPPMPPSAQGPLPPCPIRPPFPN	Дy	
E 54 R 300	8 HRMSFHPGRGCPRGRGGHGARPSAPSFRPQNLRLLHPQQPPVQYQYE	Qу	
Gaps 32;	Match 3.6%; Score 273; DB 5; Length 827; Local Similarity 24.8%; Pred. No. 4.5e-05; es 158; Conservative 54; Mismatches 216; Indels 210;	Query M Best Lo Matches	
ODS THEREOF	Sequence 17077, Application US/09935625 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al. TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS TITLE OF INVENTION: MODULATING VARIOUS RESPONSES FILE REFERENCE: 2750-1481P CURRENT APPLICATION NUMBER: US/09/935,625 CURRENT FILING DATE: 2001-08-24 NUMBER OF SEQ ID NOS: 33136 SEQ ID NO 17077 LENGTH: 827 TYPE: PRT ORGANISM: Arabidopsis thaliana FEATURE: NAME/KEY: Deptide LOCATION: 1.827 OTHER INFORMATION: Ceres Seq. ID no. 2708208	CÓ C	
	12	70	
	265 YRSDYDRGRTPSRHRSYERSRERERHRHRDNRRSPSLERSYKKEYK 312 ;  ;  ;                              ;    ; 433 EKSRHKSRSRDRHDDYYRERSRERERHRDRDRDRDRERDREREYR 478	Db Qy	
R 264   R 432	238	Qy Db	
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; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1.847
; OTHER INFORMATION: Ceres Seq.
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CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 17076
LENGTH: 847
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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          SDKLSEKRSVHRHHGSQMSPVENSEGRSRPVSSKVKD-SEQVEKEDNSDLDANLSCDSKD
                                                          GRKHQRERRSPGRLSEEQDRVQNSKLLKRTSVPDTDKRKQLPEKLLEVGRVEHYKEQERK
                                                                                  EKKRARWEEEKDRWSDNQ---SSGKDKNYTSIKEKEPEETMPDK-----NEEEEEE
                                                                                                                                 SPSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSPS-R
                                                                                                                                                               RGKSSPS-SRHQKARSPVRRRSP--
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                                   LLKPVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGS-------
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US-09-935-625-17480

Sequence 17480, Application US/09935625

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CEITTLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 17480
LENGTH: 859
LENGTH: 859
LENGTH: PRT
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; FEATURE:
; NAME/KEY: peptide
; LOCATION: 1..859
; OTHER INFORMATION: Cere
US-09-935-625-17480
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Best Local Similarity
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                                                                                                                                                                                      GRKHQRERRSPGRLSEEQDRVQNSKLLKRTSVPDTDKRKQLPEKLLEVGRVEHYKEQERK
TIRHQIKDKNRR---
                                            ---RQEKAKAARPPWEPPKTKLDEDLESSSESECESDEDSTCSSSSDSEVFDVIAEIKRK 511
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Pred. No. 4.7e-05;
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549	STCSSSSDSEVEDVIAEIKRK 511 :     :      : NGSSDSDV-DDRKEAKRR 796	DKFEEELGS 454 ::  :    EQVEKEDNSDLDANLSCDSKD 753	IMPDKNEEEEEE 406 : :  2LPEKLLEVGRVEHYKEQERK 694	KNTDSWAPPLEIVNHRSPS-R 358   :             SRSPPVLHRSPSPR 634	TPSRHRSYERSRERERERHRHRDNRR 299 	DHRHRDHSHG 239          GRHTSPSHIKQDGSMSPVRG 565	GYSHHNFPPPSFNSFQNNPS 190	PNNPPVPGAPP 137  :	PMPPSAOGPLPPCPIRPPPPN 104	HPQQPPVQYQYE 54	5; Length 879; .05; 216; Indels 210; Gaps 32;	ES, CELLS, AND METHODS THEREOF CAPABL	949 796

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## ALIGNMENTS

C;Date: 13-000 (C)Accession: T21419
C;Accession: T21419
R;Lightning, J.
submitted to the EMBL Data Library, submitted to the EMBL Data Library, submitted to the EMBL Data Library,

A; Reference number: A; Accession: T21419

A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-412 <WIL>

from GB/EMBL/DDBJ

October 1996

hypothetical protein F26E4.13 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

δÃ Qγ Ş B Q A;Cross-references: EMBL:281070; PIDN:CAB03005.1; GSPDB:GN000019; CESP:F26E4.13
A;Experimental source: clone F26E4
C;Genetics: δÃ 밁 Qy Вþ 망 QY В В A; Map position: 1 A; Introns: 359/2; 400/3 A; Gene: CESP:F26E4.13 Query Match
Best Local Similarity
Matches 181; Conserv 1183 1123 1064 FGRLLF-NDPDLREVWLNYPLHPLQLQEPNTDRQLIETSPVLQKLTEFEEAIGVIFTHVR 1122 1004 VQNQHLAMLAKKLELDPFMLYAHGPDLCRESDLRHAMANCFEALIGAVYLEGSLEEAKQL 1063 118 944 TLINIMSRLGQDDPTPSRINHNERLEFLGDAVVEFLTSVHLYYLFPSLEEGGLATYRTAI 1003 58 2 SLFNIMKGTSGGEP----ILHNERLEYLGDAVVELIVSHHLYFMLTHHFEGGLATYRTAL 57 NNRTQAKVAEELGMQEYAITNDKTKRPV---GLRTKTLADLLESFIAALYTDKDLEYVHT 1239
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SNQTQAVVCDDLGFTEFVI-----KAPYKTPELKLKDKADLVEAFIGALYVDRGIEHCRA 292 TVAVYFKGERIGCGKGPSIQQAEMGA---AMDALEKYNFPQM-AHQKRFIGRKYRQELKE 1354 LLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQLVATEYLFIHFPDHHEGHLTLLRSSLV 1182 KIAVYYKGKRLASAAESNVHKAELRVAELALANLESMSFSKMKAKNNSNMRRRLEQDTSD 412 FMNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLR-TEGKEPDIPLYKTLQTVGPSHARTY 1298 LLAKAFTRRNIPNNDLTKGHNQRLEWLGDSVLQLIVSDFLYRRFPYHHEGHMSLLRTSLV 237 VQNRNLATLAKNCRIDEMLQYSHGADLINVAEFKHALANAFEAVMAAIYLDGGLAPCDVI 117 FSKAMYGHQPVLKEKWDHINEHELKREDPQGDRDLSFITPTLSTFHALEERLGIQFNNIR 177 Conservative 11.9%; Score 890; DB 2; Length 412. 43.1%; Pred. No. 3e-40; 85; Mismatches 136; Indels 18; Gaps

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R;Lightning, J.
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F26E4.10 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: Caenorhabditis elegans hypothetical protein F26E4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Accession: T21420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Caenorhabditis elegans; Date: 15-Oct-1999 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
   603
                                                                                                                                                       491
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                                                                                                                                                                                                                                                           GKEVLSMHQILLYLL-RCSKALVPEEEIANMLQWEELEWQKYAEECKGMIVTNPGTKPSS 751
                                                                                                                                                                                                                                                                                                                      EMMP-ENFCVKGLELFSLFLFRDILELYDWNLKGPLFEDSPPCCPRFHFMPRFVRFLPDG 692
                                                                                                                                                                                                                                                                                                                                                                                                             VSPPTNFLTDRPTVIEYDDHEYIFEGFSMFAHAPL----TNIPLCKVIRFNIDYTIHFIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DELWYNDPGQMNDGPLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNNAGRLFHY--RIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEDLESSSESECESDEDSTCS-------SSSDSEVFDVIAEIKRKKAHPDRLH 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIIKNTDS-----WAPPLEIVNHRSPSREKKRARWEEEKDRWSDNQSSGKDKNYTSIK 388
YNFSLDVFEEVIEYKFNDRRVIELALMHSSFKSHYGTPIDHVKNMITNCGYRR-KYG---
                                 YHQCLMHLDKLIGYTFQDRCLLQLAMTHPSHHLNFGMNPDHARNSLSNCGIRQPKYGDRK 931
                                                                                                          QTDKQKLAQREEALQKIRQKNTMRREVTVELSSQGFWKTGIRSDVCQHAMMLPVLTHHIR 871
                                                                                                                                                   IRADWFERDEEKKEV----YVVHNAIRAQTYTAISLPRIAFLEKTLNKMIQ-EKQSSGVY
                                                                                                                                                                                                                          LVQLWSSKTVLAYFTSKGSSEIMSPEDVNRLCDAQIDQFTRNTSKHKQSIVLNTKFKPSA
                                                                                                                                                                                                                                                                                                   EFMPDECFDPEDCDMLFEYIFHEIFEMLDFELRPKHIPSDVESCPMIHIMPRFVQ-TKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GE------VKDEKQTCNRRNQQRKAKRLRNFEEKERQITLLKKGIDRKKTHPNGIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGDESFTASDVSDDSNDS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEEAEKYMMIKAKSTTSKILQDFQTKILETVKTKRRLQADVPYIIHPCHSMKGRKTPKQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSPRLTEKDYETNYMIDPP--VVSTHSAELIK--
                                                                        NKDFEK---TKNELEHLKRENRSARNLKLREPVAGFIETGLKPDVAAHVVMTILACHHIR
                                                                                                                                                                                    VRIDQLDREQFNPDVITFPIIVHFGIRPAQLSYAGDPQYQKLWKSYVKLRHLLANSPKVK 811
                                                                                                                                                                                                                                                                                                                                                                           PLPSENQL--YRTHMAINGEEFEFEGFSLITHAPLPDCMTRAPICK---YSMDYEFQLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDISFNEKGLGNEGPECRCPEPIKTCGLKHGYYAGEDKAIDCK--KSNGENLHYYTLRVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKAKAARPP--WEPPKTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KHKRARRKKYQKEYQERHKEEMMQQLGRRFQNQPSTSSAPPDTVEKIPLPTESTSALPFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119/3; 226/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative 126; Mismatches 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.48;
24.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303/2; 377/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 558; DB 2;
Pred. No. 2.7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QDEASTSEPTNRQAPEADKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 682;
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                                                                                                                         В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-551 <FLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data A; Reference number: S57447 A; Accession: S57447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NyAlternate names: HPBRII-4 protein C;Species: Homo sapiens (man) C;Date: 10-Oct-1995 #sequence_revision C;Accession: S57447; S57489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: X67337; NID: g871298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-551 <FL2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S57489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Fleischhauer, K.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPBRII-7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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 515
                               276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                       SRHRSYERSRERERHRHRDNRRSPSLERSYKKEYK 312
DRHDDYYRERSRERERHRDRD--RDRDRERDREREYR
                                                                                                                                                          PLPKAPSERRSPERLKHYDDHRHRDHS-----
                                                                                                                                                                                                                                                                                                                                                                                                               PRGRGGHGARPSAPSFRPQNLRLLHPQQPPVQYQYEPPSAPSTTFSNSPAPNF----LPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary
                                                                                                                                                                                                            MPQQVNYQYPPGYSHHNFPPPSFNSFQNNPSSFLPSANNSSSP---HFRHLPPY-----
                                                                                                                                                                                                                                                      GPPP-PVPGYGPPPGPPPPQQGPPPPPGPFPPRPPGPLGPPLTLAPPPHLPGPPPGAPPP
                                                                                                                                                                                                                                                                                    MPPPMPCPNNPPVPGAPPGQ------GTFP-----FMMPPPSMPHPPP--PPV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                 111;
                                                             QSKVSADDRCKVLISSLQDCLHGIESKSYGSGSRRERSRERDHSR--SREKSRRHKSRSR
                                                                                                                         PPGREMDTARTPLSEAEFEEIMNRNRAISSSAISRAVSDASAGDYGSAIETLVTAISLIK
                                                                                                                                                                                          AP-HVN----PAF----FPPPT
                                                                                                                                                                                                                                                                                                                                                  RPDFVPFPPPMPPSAQGPLPPCPIRPP----FPNHQMRHPFPV------PPC--FPP 119
                                                                                                                                                                                                                                                                                                                  RP---PLGPPGPPGPPGPPPGQVLPPPLAGPPNRGDRPPPPVLFPGQPFGQPPLGPLPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human
HPBRII-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL:x67336; NID:g871300;
                                                                                           -----HG-RGERHRSLDRRERGRSPDRRRQDSRYRSDYDRGRTP 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  678
                                                                                                                                                                                                                                                                                                                                                                                                                                               32;
                                                                                                                                                                                        -----NSGMPTSDSRGPPPTDPYGRPPPYDRGDYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 316; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      June
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   -VPGGDRFPGPAGP----GGPPPPFPAGQTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-Nov-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                .6e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:CAA47752.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIDN:CAA47751.1;
 549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               148;
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ribonuclease III (EC 3.1.26.3) - Bacillus subtilis
N;Alternate names: RNase D; RNase O
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 20-Jun-2000
C;Accession: B69693; JC4821

R; Kunst, F.; C.; Bron, S.;

Ogasawara, N.; Moszer, I.; Brouillet, S.; Bruschi, C.

Albertini, A.M.; Alloni, G.V.; Caldwell, B.; Capuano,

, G.; . V.;

Azevedo,

Carter,

V.; Ber , N.M.;

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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallex lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A,Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot Reuchl, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.; Zumstein, E.; Yoshikawa, H.; Danchin, A. A; Reference number: A65580; MUID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; PIDN:CAB13466.1; PID:g26339 R;Experimental source: strain 168 R;Copuro, A.; Kakeshita, H.; Takamatsu, H.; Nakamura, K.; Yamane, K. Gene 172, 17-24, 1996 Gene 172, 17-24, 1996 A;Title: The effect of Srb, a homologue of the mammalian SRP receptor alpha-subunit, A;Reference number: JC4819; MUID:96257247
                                                                                                                       ribonuclease III homolog rncS [imported] - Listeria monocytogenes (strain EGD-C;Specles: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001 C;Accession: AE1300 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: ribonuclease III; double-stranded RNA-binding repeat C;Kcywords: hydrolase F;172-245/Domain: double-stranded RNA-binding repeat homology <DSR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: rncS; srb
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A; Residues: 1-78, 'p', 80-137, 'K', 139-170, 'p', 172-242, 'E', 244-249, 'LNPPYDSGGFQYVCRLI'
A; Cross-references: DDBJ:D64116; NID:g1389548
A; Cross-references: DBBJ:D64116; NID:g1389548
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; V. A;Title: Comparative genomics of Listeria species
                             A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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A;Status: nucleic acid sequence not shown; translation not shown
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Nature 390, 249-256,
                                                                              Science 294,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues:
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                                                                                                       Jones, L.M.; Karst,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1104 LQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGH--NQRMEFLGDSIMQLVATEY 1161
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                                                                            849-852,
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6, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.2%; Score 315; DB 2; 34.7%; Pred. No. 6.8e-10; tive 46; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          release 106.0, (PID:g1389549) has 138-Glu
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                           Maitournam, A.;
Voss, H.; Wehla
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                                                                                                                                  .D.;
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                                                                                                                               ; Bloecker
Fsihi, H.
                             Wehland
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C;Superf
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A;Accession: AB1300
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-229 <GLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D: Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.
A; Title: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID:21537279; PMID:11679669
A; Accession: AE1672
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AE1672
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Accession: AE1672
C;Accession: AE1672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-229 <GLA>
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                                                                                                                                                                                                                                                                                             1109 EFEEAIGVIFTHVRLLARAFTLRTVGFNHL--TLGHNQRMEFLGDSIMQLVATEYLFIHF 1166
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Local Similarity 33.08;
                                                                                                                                                                                                                                                                                                                                                                                                  Local
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  L-YKTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALEKYNFPQMAHQ 1340
                                                                                                       IAALYTDKDLEYVHTFMNVCFFPRLK--EFILNQDWNDPKSQLQQCCLTLRTEGKEPDIP 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEYDILGETGPAHNKAFDAQVIVNGQVLGKGSGRTKKQAEQSAAQFAINK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVGLRTK--TLADLLESF 1224
                                                         IGALYLDNGIDKYVKFLERVIFPKIDAGAYLQTVDY---KTQLQEIV-----QRDRDVL 175
                                                                                                                                                                PDMAEGHMTKMRAAIVCEPSLVEFAEAVHFSKY-VRLGKGEEKAGGRTRPALLADVFESF 124
                                                                                                                                                                                                              PDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVGLRTK--TLADLLESF 1224
                                                                                                                                                                                                                                                                  ELQESVGFDFQNVELLQQAFTHSSYVNEHRRENVKDNERLEFLGDAVLELTVSDYLFNKY 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGALYLDNGIDKVVTFLERVIFPKIDAGAYLQTVDY---KTQLQEIV-----QRDRDVL 175
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Pred. No. 1.5
                                                                                                                                                                                                                                                                                                                                                                                               Score 300; DB 2;
Pred. No. 3.8e-09;
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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urget, O.; Ent
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J.A.; Voss, H.; Wehla
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K.D.; Fsihi,
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R;Witte, M.M.; Scott, R.E. submitted to the EMBL Data Library, November 1998 A; Reference number: Z22246 A; Accession: T42727 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: mRNA A; Residues: 1-1560 <WIT> A; Cross references: EMBL:U83913; NID:g3858884; PID:g3858885; PIDN:AAC72432.1 A; Experimental source: strain Balb/C C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: P2P-R
C;Function:
A;Description: in
C;Superfamily: RII
F;57-107/Domain: 1
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c;SpecLes: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 02-Sep-2000
C;Accession: T42727
R;Witte, M.M.; Scott, R.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRPDEVPEPPPMPPSAQGPLPPCPIRPPFPNHQMRHPFPVPPCFPPMPPPMPCPNNPPVP 133
 KEEATKIDSVKPSSSSQKDEKVTGT-
                                     DEDST-----CSSSSDSEVFDVIAEIKRKKAH 514
                                                                                                                                                                                                                             SHRNRNLGGNYPEKLSTRDSHNAKDNPKSKEKESENVPGDGKGNKHKKHRKRRNEEKGEE 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLKEESKFPYSGSSYSRSSYTDSKSRSGSTRSRSYSRSFSRSHSRSYSRSPPYP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GQPPTAG---YSVPPPGFPPAPANISTACESPGVPTAHSNTMPTTQAPLLSREEFYREQK 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAPPGQGTFPFMMPPPSMPHPP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKDKREKDKPKVKSDKTKRKSDGSATAKKDNVLKPSKGPQEKVDGDREKSPRSEPPLKKA
                                                                                                               LRDLYDKFEEELGSRQEKAKA---
                                                                                                                                                   SESFLNPELLGKFRKCRGSSGIDETKTDTLFVFPSREDATPVRDEPMD--AESITFKSVS
                                                                                                                                                                                           EEELLKPVWI - - - - RCTHSENY - - -
                                                                                                                                                                                                                                                                                                           YYKGYAVGAQPRPSA----
                                                                                                                                                                                                                                                                                                                                             SGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAP----PLEIVNHRSPSREKKRARWEEEK 369
                                                                                                                                                                                                                                                                                                                                                                                   K-RNVPRG-ETEREYFNRYREVPPPYDIKAYYGRSVDFRDPFEKERYREWERKYREWYEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RRGRGKSRNY---RSRSRSHG---YHRS----RSRSPPYRRYHSRSRSPQAFRGQSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----QYP---PGYSHHNFPPPSFNSFQNNPSSFLPSANNSSSPHFRHLPPYPLPKAPS 217
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                                                                                                                                                                                                                                                                   ---QSSGKDKNYTSIKEKEPEETMPD------
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23.8%; Pred. No. 1e-07;
tive 72; Mismatches 2
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--PRKAH
                                                                                                             -ARPPWEPPKTKLDEDLESSSESE---CES 487
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863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribonuclease III rncS [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
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                                                                                                                                                                                                C; Superfamily: ribonuclease III; double-stranded RNA-binding repeat
                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-263 <STO>
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C;Superfamily: ribonuclease III; double-stranded RNA-binding repeat homology
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A; Residues: 1-225 <HEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                            A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06208.1; GSPDB:G
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE004316; GB:AE003852; NID:g9657034; PIDN:AAF95603.1; A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
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                                                                                                                          Query Match
Best Local
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                                              1084 HPLQLQEPNTDRQLIETSPVLQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNH--LTLG 1141
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Local Similarity 32.2%;
tes 75; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELYRRFPKVNEGDMSRMRATLVRGNTLAELGREFDLGDYLKLGPGELKSGGFRRDSILAD
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                                                                                                . Similarity 77; Conserv
                                                                                                   Conservative
KRLTLTAKQQQMFDELLRTLNLTFANKKLLVQAFTHSSYVNEHRIQSCK 71
                                                                                                                       30.9%;
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Pred.
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Pred. No. 2.2
                                                                                                   Mismatches
                                                                                                                       No. 4
                                                                                                                          4.1e-08;
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H.; Dragoi, I.;
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ribonuclease III (EC 3.1.26.3) [imported] - Streptococcus pneumoniae (strair C;Species: Streptococcus pneumoniae C;Decies: Streptococcus pneumoniae C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001 C;Accession: F98012
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; Del e, R.; Leblanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; Mt. y. P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A;Anthors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jas A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MOID:21429245; PMID:11344234
A;Accession: F98012
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A;Gene: rncS
C;Superfamily: ribonuclease III;
                                                                                                                                                    ribonuclease III [imported] - Streptococcus pneumoniae C;Species: Streptococcus pneumoniae C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #tex C;Accession: H95144
                                                                                                                                                                                                                                                            RESULT
H95144
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F98012
                                               R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; on, J.D.; Umayam, L.A.; white, O.; Salzberg, nson, T.; Hickey, E.K.; Holt, I.E. Science 293, 498-506, 2001
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A; Molecule type: DNA
A; Residues: 1-232 <KUR>
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  A; Authors: Loftus, B.J.; Yang, F.; A; Title: Complete Genome Sequence of
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79; Conser
                                                                                                                                                                                                                                                                                                                                                         Conservative
Genome Sequence of a virulent
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Pred. No. 3.8
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                                                                                                     Eisen, J.A.;
S.L.; Lewis,
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hes 91;
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Venter, isolate
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J.C.; Dougherty,
of Streptococcus
                                                                                                     Read,
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                                                                                                                                                                                                                                  TIGR4)
                                                                                                  T.D.; Peterson, S.; Hei Radune, D.; Holtzapple,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                            24-Aug-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                homology
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, P.; McAhren,
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  pneumoniae.
                       B.A.;
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                       Morrison
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C; Superfamily: RING finger homology
C; Keywords: tandem repeat; zinc
C; Keywords: tandem repeat; zinc
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C; Superfamily:
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C;Genetics:
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A; Residues: 1-948 <SAK>
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nes 75; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                            3.7%;
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A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: H95144
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-232 <KUR>
A;Cross-references: GB:AE005672; PIDN:AAK75353.1; PID:g14972730; GSPDB:GN00164; TIGR:A;Experimental source: strain TIGR4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A57640
R;Sakai, Y.; Saijo, M.; Coelho, K.; Kishino, T.; Niikawa, N.; Taya, Y.
Genomics 30, 98-101, 1995
A;Title: cDNA sequence and chromosomal localization of a novel human protein, A;Reference number: A57640; MUID:96129310
A;Accession: A57640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           retinoblastoma binding protein RBQ-1 - human
C;Species: Homo sapiens (man)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 17-Mar-2000
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                                                                                                                                                                                                                                      PDFVPFPPPMPPSAQGPLPPCPIRPPFPNHQMRHPFPVPPCFPPMPPPMPCPNNPPVPGA 135
                                                                                                                                                                                                                                                                                        ARPGGGRPGWEHSN-KLGYLVSPPQQIRRGERSCYRSINRGRHHSERSQRTQGPS-LPAT 377
                                                                                                                                                                                                                                                                                                                                      ARPSA--PSFRPQNLRLLHPQQPPVQYQYEPPSA-----PSTTFSNSPAPNFLPPR 75
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                                                                            PPPAG---YSVPPPGFP-PAPANLSTPWVSSGVQTAHSNTIPTTQAPPLSREEFYREQRR 471
                                                                                                                              PPGQGTFPFMMPPPSMPHPPPPPVMPQQVN---
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                                                                                                                                                                                                                                                                                                                                                                                                Score 276; DB 2;
Pred. No. 4.4e-07;
1; Mismatches 208
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Pred. No. 4.8
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ches 91;
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-GYSHHNFPPPSFNS 184
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Rudd,

584/1

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A;Cross-references: EMBI
A;Experimental source: C;Genetics:
A;Map position: 4
A;Note: T9E8.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  extensin homolog T9E8.80 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 11-Jun-1999 C; Accession: T06291 To the Protein Sequence Database, April 1999 A; Reference number: Z15588 A; Accession: T06291
                                                                                                                                                                                                                                                        δã
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A; Residues: 1-760 <BEV>
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Best Local (
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 PPPPPTPVSSP
                                  -PKAPSERRSP
                                                                                                        QVNYQYPPGYSHHNFPPPSFNSFQNNP---SSFLPSANNSSSPHF----RHLPPYPL----
                                                                                                                                                CFPPM----PPPMPCPNNPPVPGAPPGQGTFPFMMPPPSMPHPPPPPV------MPQ
                                                                                                                                                                                                                        PGRGCPRGRGGHGARPSAPSFRPQNL-----RLLHPQQPPVQYQYEPPSAPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSSESECESDEDSTCSSSSDSE------VFDVIAEIKRKKAHPDRL
                                                                        PVYCTRPPPPPPPPPPQFSPPPPPPPYYYSSPPPPHSSPPPPHSPPPPPIYPYLS
                                                                                                                                                                                                                                                        ----TTFSNSPAPNFLPPRPDF-VPFPPPMPPSAQGPLPPCPIRPPFPNHQMRHPFPVPP 115
                                                                                                                                                                                                                                                                                            PGRPAQRSPGOCKAFLSRP---PVNCGSFSCGRSVSP-RPPVVTPLPPPSLPSPPPPAPI 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNDGSAVSKKENIVKPAKGPQEKVDGDVRDLLDLNLQLKKPKRRLRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EENKTDSLFVLPSRDDATPVRD--EPMDAESITFKSVSEKDKRER---DKPKAKGDKTKR 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDNTKSKEKESENAPGDGKGNKHKKHRKRRKGEESEGFLNPELLETSRK----SREPTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KNYTSIKEKEPEETMPD------KNEEEEEELLKPVWIRCTHSENYYSSDPM--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NRENFSPERFLPLNIRN--SPFTRGRREDYVGGQSHRSRNIGSNYPEKLSARDGHNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIKNTDSWAP----PLEIVNHRSPSREKKRARWEEEKDRWSDNQSSG------KD
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                  3.7%; Score 275; DB 2;
Llarity 35.1%; Pred. No. 3.8e-07;
Conservative 15; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL:AL049608 ce: cultivar Columbia;
 601
                                    222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z25009
A; Accession: T48946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 45/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position:
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A; Residues: 1-1531 <
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                  NHNERLEFLGDAVVEFLTSVHLYYLFPSLEEGGLATYRTAIVQNQHLAML--AKKLE---
                                                                                                                                                                                                                        ---KKYGIVLAH--PNQPLMKLKQSHHAHNLLVDFNEEMVVKTEPKAGNVRKRKPNI----
                                                                                                                                                                                                                                             LWKSY-VKLRHLLANSP--KVKQTDKQK---LAQREEALQKIRQK--NTMRREVTVELSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ECESDEDSTCSSSSDSEVFDVIAEIKRKKAHPDRLHDEL---WYNDPGQMNDGP-----
 FSMERLELLGDSVLKYVASCHLFLKYPDKDEGQLSRQRQSIISNSNLHRLTTSRKLQGYI 1029
                                                                                                          HLNFGMNPDHARNSLSNCGIRQPKYGDRKVHHMHMRKKGINTLINIMSRLGQDDPTPSRI 962
                                                                                                                                                                                                                                                                                                                                                                                                        CCPRFHFMPRFVRFLPDGGKEVLSMHQILLYLLRCSKALVPEEEIANMLQWEELEWQKYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KVASSKSKSSSAAGSK-----KRKELHGTTCANALSGTW----GENIDGATFQAYK 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGVKEIGSMVIPDSNITVSEEAASTQTMSD---PPSRNEQLPPCKKLRLDNNLLQSNGKE 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DST-VVGTSRLRDLYDKFEEELGSRQEKAKAARPPWE----PP--KTKLDED-LESSSES 483
                                                                      RLESLMLASQLREEI-DCSIDNFSISSTSI---
                                                                                                                                                                                QGFWKTGIRSDVCQHAMMLPVLTHHIRYHQCLMHLDKLIGYTFQDRCLLQLAMTHPS--H
                                                                                                                                                                                                                                                                                              LEELVVIAIHTGRIYSIVEAVSDSSAMSPFEVD---------ASSGYATYAEYFN
                                                                                                                                                                                                                                                                                                                                EECKGMIVTNPGTKPSSVRI--DQLDREQFNPDVITFPIIVHFGIRPAQLSYAGDPQYQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----TNNAGRLFHYRITVSPPTNFLTDRPTVIEYDDHEYIFEGFSMFAHAPLTNI 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100/3; 138/3; 183/3; 227/3; 278/3; 322/1; 357/2; 421/3; 475/2;
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                                                                                                                                                HAHLPPEL-----LARID-----VPRAVLKSIYLLPSVMH
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21.3%; Pred. No. 9.7e-07;
tive 142; Mismatches 420;
                                                                         --LEAVTTL-
                                                                                                                                                                                                                                                                                                                                                                    - LDDKMEETNLIHFANASSDKNS
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      Qy
      161 PQQVNYQYPPGYSHHNPPPPSFNSFQNNPSSFLPSANNSSSPHFRHLPP---YPLPKAPS 217

      Db
      197 GDQTT-QPPPLW----LPPPPPGD-ETPPVFSLPPPLDEFPP----MPPITWLPPPDVPA 246

      Qy
      218 ERRSPERLKH--------YDDHRHRDHSHGRGERHRSLDRREGRSPDRRRQDS 263

      Db
      247 QTSSAEAFDQIPPLVTITEAIENPHNSHRHRD-----ENKKGLDRRNR-RVKSRRRSRS 299

      Qy
      264 R 264

      Db
      300 R 300
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Search completed: October 9, 2002, 18:26:49
Job time: 58 secs

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Title:
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7486
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length: 2000000000
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SPTREMBL_19:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyright
                                                                                                                                                                                                                                          sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_virus:*
sp_vertebrate:*
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sp_bacteria:*
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1374
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588
229
1591
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                Q9XYN5
Q9YYN5
Q9Y4Y0
Q9Y4Y0
Q9Y4Y0
Q9Y1327
Q9U908
L Q9CTG2
Q9VAY4
Q16630
Q9BW18
Q92AK3
P97868
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Q9NW73
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                                                                     O9nrr4 homo sapien
O9nw73 homo sapien
O9xyn5 drosophila
O9y2v9 homo sapien
O960y4 drosophila
O9v4y0 homo sapien
O01327 caenorhabdi
O9u9q8 caenorhabdi
      O9ctg2 mus musculu
O9vay4 drosophila
O16630 homo sapien
O9bw18 homo sapien
O9bw18 homo sapien
O92ak3 listeria in
P97868 mus musculu
O9sbm1 volvox cart
                                                                                                                                                         Description
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009084 lycopersico Q9ull5 homo sapien Q9esu6 mus musculu Q9lj64 arabidopsis	Q09084 Q9ULL5 Q9ESU6 Q9LJ64	10 4 11	322 1217 1400 956	0 0 0 0 0 4 4 0 0	259 258 256	443
Q9fpq Q9fpq Q9fpq	Q9C012 Q9FPQ6	10	1236 555		259.5	40
013849 Q96u76	Q96U76	<b>υ</b> ω ω	740 763	ა	265 265	38
001864 0948y7	001864 Q948Y7	10	988 687	. w w	267	36
Q99un7	Q99UN7	16	243	3.6	267	34
Q931t1 09pm40	Q931T1	16 16	243 224	 ი ი	268 267	332
000302	000302	<b>.</b> ~ (	884	3.6	269	31
Q9a105	Q9A105	٦ <u>6</u>	230	ν ω 	271.5	200
Q9vsh4 c	Q9VSH4	σ	702	3.6	272.5	28
Q9fy:	Q9FYB2	10	894	ω. 6	273	27
Q91mq1	Q9LMQ1	10	1006	•	273.5	25
Q91xw7	Q9LXW7	10	1531		274.5	24
Q9t0k5	Q9T0K5	10	760	3.7	275	23
Q9vep4	Q9VEP4	σ,	594	3.7	275.5	22
015290 015290	015290	4 5	948	3 . 7	2/9.5	21
Q9ka05	Q9KA05	16	263	ω	282	19
Q96ph3	Q96РН3	4	1616	3.8	284.5	18
Q95ts9	Q95TS9	ر.	652	3. 8	285	17

## ALIGNMENTS

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RESULT 1
Q9NRR4
                                                                                                                                                                      ID DAG GOOG DEFINATION OF THE PROPERTY OF THE 
    Query Match
Best Local Similarity
Matches 1372; Conserva
                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-20538440; PubMed=10948199;
MU H., Xu H., Miraglia L.J., Crooke S.T.;
"Human RNase III is a 160-kDa protein involv
processing.";
J. Biol. Chem. 275:36957-36965(2000).
EMBL; AF189011; AAF80558.1; -
InterPro; IPR001159; DS_RBD.
InterPro; IPR001159; DS_RBD.
InterPro; IPR009955; P_rich_extensn.
InterPro; IPR009999; RNase_3.
Pfam; PF00035; Gsrm; 1.
Pfam; PF00035; RIBOcnuclease_3; 2.
Pfam; PF00035; PRICHETTENSN.
SMART; SM00358; DSRM; 1.
SMART; SM00358; DSRM; 1.
PROSITE; PS001317; DS_RBD; 1.
PROSITE; PS00137; DS_RBD; 1.
PROSITE; PS00137; RNASE_3_1; 2.
PROSITE; PS00142; RNASE_3_2; 2.
SEQUENCE 1374 AA; 159244 MW; 88810852391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9NRR4 PRELIMINARY; PRT; 1374 AA.
Q9NRR4; O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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        Conservative
                                         99.8%;
pred. No. 0;
0; Mismatches
                                                                                                                                                                  888108523912F705 CRC64;
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                                                                              DB 4;
    2;
                                                                          Length 1374;
    Indels
    0;
    Gaps
    0;
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Q9BSJ7

homo

sapien

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1 MMQGNTCHRMSFHPGRGCPRGRGGHGARPSAPSFRPQNLRLLHPQQPPVQYQYEPPSAPS 60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLSYAGDPQYQKLWKSYVKLRHLLANSPKVKQTDKQKLAQREEALQKIRQKNTWRREVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                   KRARWEEEKDRWSDNQSSGKDKNYTSIKEKEPEETMPDKNEEEEEEELLKPVWIRCTHSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSPSREK
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                                                                                                                                                                                                                  NMLQMEELEWQKYAEECKGMIVTNPGTKPSSVRIDQLDREQFNPDVITFPIIVHFGIRPA
                                                                                                                                                                                                                                                      DWNLKGPLFEDSPPCCPRFHFMPRFVRFLPDGGKEVLSMHQILLYLLRCSKALVPEEEIA
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RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishid S., Kawai Y., Saito K.,
RA Yamamotto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwayanagi T.;
RY "NEDO human cDNA sequencing project.";
RT "NEDO human cDNA sequencing project.";
RT "WEDO human cDNA sequencing project.";
RI Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

DR RHEL; AKOO1121; BAA91511.1; -.
DR RHEL; AKOO1121; BAA91511.1; -.
DR RHEL; ROUGAS; RIBOUS, DS.RBD.
DR InterPro; IPR00039; DS.RBD.
DR InterPro; IPR00039; DS.RBD.
DR Pfam; PF00635; Ribonuclease_3; 2.
DR Pfam; PF00635; RIBOC; 2.
DR SMART; SM00535; RIBOC; 2.
DR PROSITE; PS50142; RNASE_3_1; 2.
DR PROSITE; PS50142; RNASE_3_1; 2.
DR PROSITE; PS50142; RNASE_3_1; 2.
SQ SEQUENCE 769 AA; 89706 MW; C92261C723C047FA CRC64;
                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9NW73 PRELIMINARY; PRT; 769 AA.
Q9NW73;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 89.7 KDA PROTEIN.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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               786
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                                                                                                                                                                                                        Local Similarity
nes 765; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITNDATKRANGLESFIAALKIDKDLESVHIFMNVCFFPRLKEFILNQDWND 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPLHPLQLQEPNTDRQLIETSPVLQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTL
                                                      EELEWQKYAEECKGMIVTNPGTKPSSVRIDQLDREQFNPDVITFFIIVHFGIRPAQLSYA 785
                                          EELEWQKYAEECKGMIVTNPGTKPSSVRIDQLDREQFNPDVITFPIIVHFGIRPAQLSYA
                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                   54.3%;
99.5%;
                                                                                                                                                                                                      Score 4071; DB 4;
Pred. No. 3.5e-281;
0; Mismatches 4;
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                                                                                                                                                                                                                                  Length
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PORTER

RESULT

RESULT
                                                      A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Istards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Stotton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Belson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Devancalista C. Ferrara C. Ferriara S., Fleischmann W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999
01-NOV-1999
01-JUN-2001
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1266
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                                          K.J.,
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9 (TrEMBLrel. 12, 1
1 (TrEMBLrel. 17, 1
       Gabrielian A.E., Garg N.S.,
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   Evangelista C.C., Ferraz C., Ferriera S., abrielian A.E., Garg N.S., Gelbart W.M., G
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       Glasser
                                      Fleischmann
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Lalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Liang Y., Lin X.,
RA McLiu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McHson D.R., Nelson K.A., Nixon K., Nusskern D.R., McShrefi A.,
RA McHson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhan G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter T.,
RI Science 287:2185-2195(2000).
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Best Local 9
Matches 621
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InterPro; IPR001159; DS_RBD.
InterPro; IPR000999; RNase_3.
Pfam; PP00035; dsrm; 1.
Pfam; PP00636; Ribonuclease_3; 2
SMART; SM00358; DSRM; 1.
SMART; SM00535; RIBOC; 2.
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS50142; RNASE_3_1; 1.
PROSITE; PS50142; RNASE_3_2; 2.
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Fillppov V.A., Fillppova M.A.
"The complete sequence of Dro.
RNASE III signatures.",
Submitted (DEC-1998) to the E
EMBL; ABD03839, AAF59169 1; -
EMBL; AF116572; AAD31170.1; -
FiyBase; FBgn0026722; drosha.
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                                  PVWIRCTHSENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKAKAARPPWEPP
                                                                     ETLEKTRAKPKVETERDRLLRQWCSNFC---
                                                                                         PSREKKRA--RWEEEKDR----WSDNQSSGKDKNYTSIKEKEPEETMPDKNEEEEEELLK
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                                                                                                                                         AHRQAKGSQHGY---YGSAARN-----
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Q960Y4
Q960Y4;
01-DEC-2001
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Mammalia; Eutheria;
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                     PRELIMINARY;
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Primates;
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Created)
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Pred. No. 2.8e
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Query Match
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EMBL; AY051775; AAK93199.1; -.
EMBL; AY051775; AAK93199.1; -.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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STRAIN-Y, CN BW SP;
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VLQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQLVATEYL
                           LFFMFPELEEGGLATYRAAIVQNQHLALLAKKLQLEEFMLYAHGSDLCHELELRHAMANC
                                                                                                                      LYYLFPSLEEGGLATYRTAIVQNQHLAMLAKKLELDPFMLYAHGPDLCRESDLRHAMANC
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545; Conservative
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Pred. No. 2.4e-
69; Mismatches
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2.4e-191;
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Plasmid.
NON_TER 1 1
NON_TER 380 380
SEQUENCE 380 AA; 44577 M
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Gunther M., Laithier M., Brison O.;
"A set of proteins interacting with transcription
identified in a two-hybrid screening.";
Mol. Cell. Biochem. 210:131-142(2000).
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01-NOV-1999
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Mammalia; Eutheria;
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Plasmid pactII.
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 EDLESSSESECESDEDSTCSSSSDSEVFDVIAEIKRKKAHPDRLHDELWYNDPGQMNDGP
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44577 MW;
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Primates;
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Best Local Sim
Matches 364;
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Pfam; PF00035; dsrm; 1.

Pfam; PF00636; Ribonuclease_3; 2.

Pfam; P00636; Ribonuclease_3; 2.

SMART; SM0035B; DSRM; 1.

SMART; SM0053B; RIBOC; 2.

PROSITE; PS50137; DS_RBD; 1.

PROSITE; PS50137; DS_RBD; 1.

PROSITE; PS00517; RNASE_3_1; 2.

PROSITE; PS00517; RNASE_3_2; 2.

SEQUENCE 1086 AA; 125333 MW; 4
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O01327; 01-JUL-1997 (Tremblrel. (
01-OCT-2001 (Tremblrel. 1
01-DEC-2001 (Tremblrel. 1
F26E4.10 PROTEIN.
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InterPro;
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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EMBL; Z81070; CAB03006.3;
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   DELWYNDPGQMNDGPLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNNAGRLFHY--RIT
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                                                                                                                                                                                                                                                                                                                                                                    RHRSYERSRERERHRHRDNRRSPSLERSYKKEYKRSGRSYGLSVVPEPAGCTPELP-G 335
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                                                                                                                 GGDESFTASDVSDDSNDS-----
                                                                                                                                                  ---ENYYSSDPMDQVGDSTVVGTSRLRDLYDKFEEELGSRQEKAKAARPP--WEPPKTKL
                                                                                                                                                                                    AEEAEKYMMIKAKSTTSKILQDFQTKILETVKTKRRLQADVPYIIHPCHSMKGRKTPKQK
                                                                                                                                                                                                                          EKEPEETMPDKNEEEEEELLK-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                         -VKDEKQTCNRRNQQRKAKRLRNFEEKERQITLLKKGIDRKKTHPNGIH
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                                                                                                                                                                                                                                                                                                                                                                                                                       19.3%; Score 1448; DB 5; 31.2%; Pred. No. 2.7e-94;
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                                     RIBONUCLEASE (FRAGMENT).
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                        01-MAY-2000 (TremBLrel.
01-MAY-2000 (TremBLrel.
01-DEC-2001 (TremBLrel.
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PRELIMINARY;

PRT;

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Created)
Last sequence up

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Rhabditida;

Rhabditoidea;

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KTLQTVGPSHARTYTVAVYFKGERIGCGKGPSIQQAEMGAAMDALEKYNFPQMAHQKRFI 1344
                                                                                                                                                                               EFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQLVATEYLFIHFPD
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Pfam; PF00636; Ribonuclease_3; 2.
SMART; SM00338; DSRM; 1.
SMART; SM00335; RIBOC; 2.
PROSITE; PS50137; DS_RBD; 1.
PROSITE; PS00517; RNASE_3_1; 2.
PROSITE; PS50142; RNASE_3_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CB1489 HIM-8(E1489);
MEDLINE-20179701; PubMed-10713462;
Filippov V., Solovyev V., Filippova M., Gill S.S.;
Filippov V., Solovyev V., Filippova M., Gill S.S.;
Falippov V., Solovyev V., Filippova M., Gill S.S.;
Falippov V., Solovyev V., Filippova M., Gill S.S.;
Theory of RNase III family proteins in eukaryotes.";
Gene 245:213-221(2000).
EMBL; AF160248; AAD45518.1; -.
InterPro; IPR001159; DS_RBD.
InterPro; IPR001999; RNase_3.

Theory of RNASE_3.
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HAMANCFEALIGAVYLEGSLEEAKQLFGRLLF-NDPDLREVWLNYPLHPLQLQEPNTDRQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDRKKTHPNGIHPDISFNEKGLGNEGPECRCPEPIKTCGLKHGYYAGEDKAIDCK--KSN
                                                                      LIETSPVLQKLTEFEEAIGVIFTHVRLLARAFTLRTVGFNHLTLGHNQRMEFLGDSIMQL
                                                                                                                                                                                           HALANAF EAVMAAIYLDGGLAPCDVIF SKAMYGHQPVLKEKWDHINEHELKREDPQGDRD
                                                                                                                                                                                                                                                               LIVSHHLYFMLTHHFEGGLATYRTALVQNRNLATLAKNCRIDEMLQYSHGADLINVAEFK
                                                                                                                                                                                                                                                                              CGYRR-KYGAEDKR---EKKRVAGIMSLFNIMKGTSGGEP----ILHNERLEYLGDAVVE
                                                                                                                                                                                                                                                                                                                                                         CGIRQPKYG--DRKVHHMHMRKKGINTLINIMSRLGQDDPTPSRINHNERLEFLGDAVVE
                                                                                                                                                                                                                                                                                                                                                                                                      VVMTTLACHHIRYNFSLDVFEEVIEYKFNDRRVIELALMHSSFKSHYGTPIDHVKNMITN
                                                                                                                                                                                                                                                                                                                                                                                                                              AMMLPVLTHHIRYHQCLMHLDKLIGYTFQDRCLLQLAMTHPSHHLNFGMNPDHARNSLSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIO-EKOSSGVYNKDFEK----TKNELEHLKRENRSARNLKLREPVAGFIETGLKPDVAAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRHLLANSPKVKQTDKQKLAQREEALQKIRQKNTMRREVTVELSSQGFWKTGIRSDVCQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIVLNTKFKPSAIRADWFERDEEKKEV----YVVHNAIRAQTYTAISLPRIAFLEKTLNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIVTNPGTKPSSVRIDQLDREQENPDVITEPIIVHEGIRPAQLSYAGDPQYQKLWKSYVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPREVQ-TKDDLVQLWSSKTVLAYFTSKGSSEIMSPEDVNRLCDAQIDQFTRNTSKHKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FMPRFVRFLPDGGKEVLSMHQILLYLL-RCSKALVPEEEIANMLQWEELEWQKYAEECKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -YSMDYEFQLVEEFMPDECFDPEDCDMLFEYIFHEIFEMLDFELRPKHIPSDVESCPMIH
                                                      IVSDFLYRRFPYHHEGHMSLLRTSLVSNQTQAVVCDDLGFTEFVI-----KAPYKTPELK
                                                                                                                      {	t LSFITPTLSTFHALEERLGIQFNNIRLLAKAFTRNIPNNDLTKGHNQRLEWLGDSVLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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36.2%;
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Pred. No. 3.2e
73; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B339A3E7C9622A08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193
                                                                                                                                                                                                                                                                                                1037
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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Rojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casawant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Slake J., Boffelli D., Bojunga N., Carninol P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Mazzarelli J., Mombaerts P.,
RA Gustincich S., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                          Query Match
Best Local S
Matches 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9CTG2;
Q9CTG2;
01-JUN-2001
01-JUN-2001
                                                                                                                                     1241 MNVCFFPRLKEFILNQDWNDPKSQLQQCCLTLRIEGKEPDIPLYKTLQTVGPSHARTYTV 1300
                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1333
                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001159; DS_RBD. Pfam; PF00035; dsrm; 1. SMART; SM00358; DSRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).

Morazoa, Chordata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1110013A17RIK PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1274
                                  1361
                                                                                                    1301
                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length Nature 409:685-690(2001).
EMBL: AK003651; BAB22917.1; .
MGD: MGI:1915895; 1110013A17Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wynshaw-Boris A
Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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121
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                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPSSSEPDMPEYRVLGIEGPTNNRIFKIAVYYKGKRLASAAESNVHKAELRVAELALA--
HQEREPEEAEDIKK
                  HQEREPDETEDIKK
                                                                 AVYFKGERIGCGKGPSIQQAEMGAAMDALEKYNFPQMAHQKRFIGRKYRQELKEMRWERE 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFPQMAHQKRFIGRKYRQELKEMRWEREHQEREPDETED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LKDKADLVEAFIGALYVDRGIEHCRAFIRIVFCPRLKHFIESEKWNDAKSHLQQWCLAMR
                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                               PS50137; DS_RBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shinagawa A., Shibata K.,
                                                                                                                                                                                                                                                                                134 AA; 15883 MW;
                                                                                                                                                                                                            Conservative
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                                  1374
                                                                                                                                                                                                                           9.5%;
                                                                                                                                                                                                          1;
                                                                                                                                                                                                                            Score 711; DB 11;
Pred. No. 4.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                 72AA673BFDC8A1C6
                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoshino M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134
                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Itoh M.,
                                                                                                                                                                                                                                                                                 CRC64;
                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                              Indels
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Absayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Patcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glann P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glann P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Glann P., Harris M.,
RA Harris N.L., Harvey D., Heinan T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kilp D., Lai Z.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kilp D., Lai Z.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kilp D., Lai Z.,
RA Harris N.L., Harvey D., Kraft C., McLod M.P., McBreson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Sinders R.D.C., Scheleter F., Shen H.,
Ra Maris N., Welssenbach J.,
Ra Maris 
                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                      Interpro; IPRUUZYUJ, ...
PRINTS; PRO1217; PRICHEXTENSN.
SEOHENCE 1151 AA; 125450 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG5514 PROTEIN.
                                      83
                                                                                                                                                                         28
PPMPPSAQGPLPPCP--IRPPFPNHQMRH9FPVPPCFPPMPPPMPCPN--NPPVPGAP-- 136
                                                                                                      RPASPKVEPP-----PPAPPGVESPPGPQPPASPRFDPPPHTIEPPPPPAPPTLVPPP 415
                                                                                                                                                                      RPSAPSFRPQNLRLLHPQQPPVQYQYEPPSAPSTTFSNSPAPNFL-----PPRPDFVPFP 82
                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel.
                                                                                                                                                                                                                                     4.5%;
ilarity 22.5%;
Conservative 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13,
13,
17,
                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                     Score 340; DB
Pred. No. 2.1e
93; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence up
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                                                                                                                                                                                                                                                                                                     Length 1151;
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VTHF-EENTDE--
                              TIHFIEEMMPENECVKGLELESLELERDILELYDW-----NLKGPLEED 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPAPPTIKPPPPPAPPTVEPPPP-----PPPAPPTVEPPPPPPAPTKVEPPPPPAPAE 469
                                                                                          RLFHYRITVSPPTNFLTDRPTVIEYDDHEYIFEGFSMFAHAPLTNIPLC--KVIRFNIDY
                                                                                                                                                        RKKAHPDRLHDELWYNDPGOMNDGPLCKCSAKARRTGIRHSIYPGEEAIKPCRPMTNNAG
                                                                                                                                                                                       QSHDRAESSKHEPEDIDGKEADNQPEKTELEARQDE-CASQNEVPTVEPQTLADSVPDLP
                                                                                                                                                                                                                    QEKAKAARPPWEPPKTKLDEDLESSSESECESDEDSTCSSSSD-----SEVFDVIAEIK
                                                                                                                                                                                                                                                     QPEDSAATMKSDAPVENANGTNGNSNGSTNGACDNVSGVVIVSDILQQSTSSFVELTAGS
                                                                                                                                                                                                                                                                                   EEEEE----LLKPVWIRCTHSENYYSSDPMDQVGDS---TVVGTSRLRDLYDKFEEELGSR
                                                                                                                                                                                                                                                                                                                 KDHDRGRDRNKSNTSGSAENKAIHDDHSESKEKYKQRRGSDSNDEGKPPSSGGPAKNS
                                                                                                                                                                                                                                                                                                                                                 WEEEKDRWSD---NQSSGKDKN----YTSIKE-----KEPEETMPDKNE
                                                                                                                                                                                                                                                                                                                                                                                 HKSSSSSRSERDKG-----KEKDKEREKDSQSRS-----HHSSSSSSSSSRR
                                                                                                                                                                                                                                                                                                                                                                                                               ----EYKRSGRSYGLSVVPEPAGCTPELPGEIIKNTDSWAPPLEIVNHRSPSREKKRAR
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                                                             ----ENPPEECVDEPAQVGDVEDP------PQDADKPATPVPISNEQSDEFSADF
                                                                                                                                                                                                                                                                                                                                                                                                                                                SSSSSKHSSSNSSSSKHKSSSSSKNDKSSSSSSSSRSNRESSSSKRSGTTSSSRHESSSHKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETRDKPHNVNTDVKEDEQPATTEDKQDKPLELGLDAPKDAVSTASESTESPTSTSSQS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----SHHNE------PPPSFNSFQNNP----
                                                                                                                           -----KVETNVEEN--KSEEESKP-----
FRTRLQLINQLIEDRKNLLNRLSED
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RESULT Q16630 ID Q16630 OT DT Q170 OT DT Q170 OT DT Q170 OT DT Q170 OT Q170 OT
Query Match
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01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                            InterPro; IPR000504; RRM.

pfam; pF00076; rrm; 1.

SMART; SM00360; RRM; 1.

PROSITE; PS50102; RRW; 1.

SEQUENCE 551 AA; 59208 MW;
                                                                                                                                                                                                                                                                                   Submitted (JUN-1995) to tl
EMBL; X67337; CAA47752.1;
EMBL; X67336; CAA47751.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Fleischhauer K.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPBRII-4 MRNA.
HPBRII-4 OR HPBRII-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q16630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01, Created)
01, Last sequence update)
17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00076; rrm; 1.
PRINTS; PR01211; PRICHEXTENSN.
SMART; SM00350; RRM; 1.
PROSITE; PS50102; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN 2001 (TrembLrel. 17, Created)
01-JUN-2001 (TrembLrel. 17, Last sequence update)
01-DEC-2001 (TrembLrel. 19, Last annotation update)
SIMILAR TO CLEAVAGE AND POLYADENYLATION SPECIFIC FACTOR 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT
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InterPro; IPR000504; RRM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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nes 111; Conserv
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                                                                                                                                                                                                                        PRGRGGHGARPSAPSFRPONLRLLHPQQP--PVQYQYEPPSAPSTTFSN---SPAPNFL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AP-HVN----PAF----FPPPT-----NSGMPTSDSRGPPPTDPYGRPPPYDRGDYG
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                          HQMRHPFPV--
                                                                         TRIPWHMGHSIEEIPIFGLKAGQTPPRP----PLGPPGPPGPPPPPGQVLPPPLAGPPN
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                                                                                                                                                                         PQGGRGRGRFPGAV---PGGDRFPGPAGPGGP----
                                                                                                                                                                                                                                                                            116;
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                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                               4.18;
                                                                                                                                                                                                                                                                                                                                                                                63470 MW;
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                          PPC--FPPMPPPMPCPNNPPVPGAPPGQ
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                                                                                                                     -PPRPDFVPFPPPMPPSAQGPLPPCPIRPP----FPN 104
                                                                                                                                                                                                                                                                       Score 306.5; DE Pred. No. 2e-13; 0; Mismatches 1
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A Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
A Bentian K.-D., Fishi H., Garcia-del Portillo F., Garrido P.,
A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
A Jones L.-M., Matournam A., Mata Vicente J., Ng E., Nedjari H.,
A Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
A Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
Comparative genomics of Listeria species.";
Science 294:849-852(2001).

BEL; AL596170; CAC97149.1; -.
                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                        Matches
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Q92AK3;
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RNCS OR LIN1919.
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01-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus/Staphylococcus NCBI_TaxID=1642;
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Bacteria; Firmicutes;
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IGALYLDNGIDKVVKFLERVIFPKIDAGAYLQTVDY---KTQLQEIV----
                              IAALYTDKDLEYVHTFMNVCFFPRLK--EFILNQDWNDPKSQLQQCCLTLRTEGKEPDIP 1283
                                                           {\tt PDMAEGHMTKMRAAIVCEPSLVEFAEAVHFSKY-VRLGKGEEKAGGRTRPALLADVFESF}
                                                                             PDHHEGHLTLLRSSLVNNRTQAKVAEELGMQEYAITNDKTKRPVGLRTK--TLADLLESF 1224
                                                                                                                           ELQESVGFDFQNVELLQQAFTHSSYVNEHRRENVKDNERLEFLGDAVLELTVSDYLFNKY
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1 (TrEMBLrel. 19,
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                                                                                                                                                                                     Score 300; DB 16;
Pred. No. 1.5e-13;
3; Mismatches 88
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"PACT: cloning and characterization of the control of t
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    CONFLICT
                                                 CONFLICT
CONFLICT
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DOMAIN
DOMAIN
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SMART; SM00184; RING; 1.

PROSITE; PS00518; ZINC_FINGER_C3HC4; FALSE_NEG.

PROSITE; PS00518; DINC_FINGER_C3HC4; PALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The proliferation potential protein-related (P2P-R) gene with domains encoding heterogeneous nuclear ribonucleoprotein association and Rb1 binding shows repressed expression during terminal differentiation."; Proc. Natl. Acad. Sci. U.S.A. 94:1212-1217(1997).
                                                                                                                                                                                                                                                                                                                                   NOT DURING THE TERMINAL DIFFERENTIATION
-!- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC
EMBL; U83913; AAC72432.1; -.
EMBL; U83913; AAC49620.1; -.
MGD; MGI:894835; Rbbp6.
InterPro; IPR001841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/C; TI
MEDLINE=97163396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BALB/C;
Witte M.M., Scott R.E.;
                                                                                                                        VARSPLIC
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                                                                                                                                                                                                                 Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISOFORM 2; MAY BE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN TESTIS.
MODERATE LEVELS FOUND IN HEART, LUNG, LIYER AND SKELETAL A
VERY LOW LEVELS DETECTED IN KIDNEY, BRAIN AND SPLEEN, ALSO
VERY LOW LEVELS DETECTED IN KIDNEY, BRAIN AND SPLEEN, ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: NUCLEAR.
ALTERNATIVE PRODUCTS: TWO ISOFORMS; ISOFORM 1 (SHOWN HERE)
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F -> I (IN REF. 1).

RQ -> GR (IN REF. 1).

H -> P (IN REF. 1).

S -> F (IN REF. 1).

S -> V (IN REF. 1).
                                                                                                                 ARG/SER-RICH.
LYS-RICH (BASIC).
MISSING (IN ISOFORM 2).
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D IN GROWTH CONTROL
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V--IAEIKRKKAHPDR--LHDELWYNDPGQ--MNDGPLCKCSAKARR
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                                                   ATAKKDNVLKPSKGPQEKVDGDREKSPRSEPPLKKAKEEATKIDSVKPSSSSQKDEKVTG
                                                                                                                                                 TKTDTLFVLPSRDDATPVRDEPMD--AESITFKSVSDKDKREKDNPKVKSDKTKRKSDGS
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                                                                                             ARPPWEPPKTKLDEDLESSSESE---CESDEDST-----
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                                                                                                                                                                   GQPPPAG---YSVPPPGFP-PAPANISTPWVSSGVQTAHSNTIPTTQAPPLSREEFYREQ
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RSGSTRSRSYSRSFSRSHSRSYSRSPPYP-----RRGRGKSRNY---RSRSRSHG---
                                         NSFONNPSSFLPSANNSSSPHFRHLPPYPLPKAPSERRSPERLKHYDDHRHRDHSHGRGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20044763; pubMed=10574980; Ender F., Hallmann A., Amon P., Sumper M.; Ender F., Hallmann A., Amon P., Sumper M.; Response to the sexual pheromone and wounding in the green alga Volvox: induction of an extracellular glycoprotein consisting almost volvox: induction of an extracellular glycoprotein consisting almost exclusively of hydroxyproline."; J. Biol. Chem. 274:15903-35028(1999).

EMBL: AJ242540; CAB62280.1; -.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP PRECURSOR.
HRGP GENE.
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InterPro; IPR003882; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01218; PSTLEXTENSIN.
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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                                                                                                                                                                                                                 Local Similarity
85 MPPSAQGPLPPCPIRPPFPNHQMRHPFPVPPCFPPMPPPMPCPNNPPVPGAPPGQGTFPF 144
                                                                                                                   31 APSFRPQNLRLLHPQQPPVQYQYEPPSA--PSTTFSNSPAPNFLPPRPDF----VPFPPP 84
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                                                           APARKPP-----PRRSPVVALVETPAAPPPGSPPPGTPPPGVPPPTPSGPEHPPPPPPP 72
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                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                        1
18
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                                                                                                                                                                                                                                                                                                                                        409
                                                                                                                                                                                                                                                                                                         41547 MW;
                                                                                                                                                                               3.8%; Score 285; DB 10; 38.4%; Pred. No. 4.1e-12; tive 11; Mismatches 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----NASTTKEPSEK-----LESTSSKIKQEKVKGK 1052
                                                                                                                                                                                                                                                                                                     HYDROXYPROLINE-RICH GLYCOPROTEIN DZ-HRGP; CD0749C6AF02BD74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----DYTSTSSTGGSPVR 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                       Length 409;
                                                                                                                                                                                  Indels
                                                                                                                                                                                  32;
                                                                                                                                                                                  Gaps
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173
             205
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PPSPPPSPPPSPPPPP
             RHLPPYPLPKAPSERRSP 222
                          MMPPPSMPHPPPPPVMPQQVNYQYPPGYSHHNFPPPPSFNSFQNNPSSFLPSANNSSSPHF
190
                                        204
                                                      119
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